

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2002, 01:51:48 : Search time 29.11 Seconds

(without alignments)  
751.685 Million cell updates/sec

Title: US-09-854-280-3

Perfect score: 1073  
Sequence: 1 MTLPGLLFLTLWHTCLAHN.....FHTEFHVPYCCTCPLRSV 197

Scoring table: BIOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 11073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq\_032802:\*

- 1: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT:\*
- 2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT:\*
- 3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT:\*
- 4: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT:\*
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- 11: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT:\*
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- 18: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT:\*
- 19: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:\*
- 20: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT:\*
- 21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:\*
- 22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1073	100.0	197	21	AA18911
2	1073	100.0	197	21	AA18911
3	1073	100.0	197	21	AA18911
4	1073	100.0	197	21	AA18911
5	1073	100.0	197	21	AA18911
6	1073	100.0	197	21	AA18911
7	1073	100.0	197	21	AA18911
8	1073	100.0	197	21	AA18911
9	1073	100.0	197	21	AA18911
10	1073	100.0	197	21	AA18911
11	1073	100.0	197	21	AA18911

12	1063	99.1	227	22	AAE08676	Human Interleukin
13	1061	98.9	227	22	AAE08680	Human Interleukin
14	1061	98.9	227	22	AAE08682	Human Interleukin
15	1060	98.8	227	22	AAE08681	Human Interleukin
16	1060	98.8	227	22	AAE08685	Human Interleukin
17	1059	98.7	227	22	AAE08684	Human Interleukin
18	1059	98.7	227	22	AAE08687	Human Interleukin
19	1058	98.6	227	22	AAE08679	Human Interleukin
20	1058	98.6	227	22	AAE08683	Human Interleukin
21	1058	98.6	227	22	AAE08686	Human Interleukin
22	1055	98.3	227	22	AAE08690	Human Interleukin
23	1054	98.2	227	22	AAE08688	Human Interleukin
24	1054	98.2	227	22	AAE08696	Human Interleukin
25	1054	98.2	227	22	AAE08691	Human Interleukin
26	1054	98.2	227	22	AAE08693	Human Interleukin
27	1054	98.2	227	22	AAE08695	Human Interleukin
28	1054	98.2	227	22	AAE08697	Human Interleukin
29	1054	98.2	227	22	AAE08699	Human Interleukin
30	1054	98.2	227	22	AAE08701	Human Interleukin
31	1054	98.2	227	22	AAE08703	Human Interleukin
32	1053	98.1	227	22	AAE08692	Human Interleukin
33	1053	98.1	227	22	AAE08694	Human Interleukin
34	1053	98.1	227	22	AAE08696	Human Interleukin
35	1053	98.1	227	22	AAE08698	Human Interleukin
36	1053	98.1	227	22	AAE08700	Human Interleukin
37	1053	98.1	227	22	AAE08702	Human Interleukin
38	1054	96.4	223	22	AAE08677	Human mature Inter
39	459	42.8	87	21	AA153890	Partial amino acid
40	459	42.8	87	22	AA666119	Human Interleukin
41	446	41.6	123	21	AA18911	Human Interleukin
42	446	41.6	123	21	AA18911	Human Interleukin
43	199	18.5	202	21	AA18911	Human Interleukin
44	199	18.5	202	21	AA18911	Human Interleukin
45	199	18.5	202	21	AA18911	Human Interleukin

## ALIGNMENTS

### RESULT 1

AA18911 standard; Protein; 197 AA.

AA18911;

08-FEB-2001 (first entry)

A novel polypeptide designated PRO1122.

Secreted protein; transmembrane protein; PRO1484; PRO4334; PRO1122;  
PRO1889; PRO1890; PRO1887; PRO1785; PRO4353; PRO4405; PRO4356;  
PRO4352; PRO4380; PRO4354; PRO4408; PRO5737; PRO5990; PRO6030;  
PRO4424; PRO4422; PRO4420; PRO4430; PRO4425; PRO5990; PRO6030;  
Insulinemia; kidney disorder; Bergers disease; nephropathy;  
Schonlein-Henoch purpura; celiac disease; dermatitis herpetiformis;  
Crohns disease.

Homo sapiens.

Key	Location/Qualifiers
Region	1..18
Modified-site	/note="signal peptide"
Modified-site	/note="leucine zipper pattern"
Modified-site	/note="N-myristoylation site"
Modified-site	/note="N-myristoylation site"
Modified-site	/note="tyrosine kinase phosphorylation site"
Modified-site	133..139
Modified-site	WO200056889-A2.



Db 121 pklafaeclctgcidartgretaaalnsrvllgslvlrrpcsrqsglprpgafafht 180  
 Oy 181 EFHVPVGCCTVLP RSV 197  
 |||||  
 Db 181 efihvpqctcvlprsv 197

## RESULT 3

AA07684  
 ID AAB07684 standard; Protein: 197 AA.

AC AAB07684;  
 DT 07-NOV-2000 (first entry)

DE A human interleukin-171 polypeptide.

KW Interleukin; IL-171; cytokine; CTLA-8; IL-17; IL-175; IL-172; IL-173;  
 IL-174; IL-176; IL-177; cell proliferation; cancer.

OS Homo sapiens.

FT Key Location/Qualifiers  
 Peptide 1..17

FT Protein /note= "signal peptide"  
 18..197

FT Modified-site /note= "mature protein"  
 55..57  
 FT /note= "putative glycosylation site"

PN WO200042187-A1.

PD 20-JUL-2000.

PE 10-JAN-2000; 2000WO-US00005.

PR 11-JAN-1999; 99US-0229402.

XX (SCHE ) SCHERING CORP.

PI Gorman DM, Bazan JF, Kastelein RA;

DR WPI: 2000-476060/41.  
 N-PSDB: AAA59149.

PT New DNA sequence encoding a mammalian homolog of CTLA-8, designated  
 Interleukin-171 (IL-171), useful for recombinant production of IL-171  
 PT which can be used for treating conditions associated with abnormal  
 PT physiology or development

PS Claim 11; Page 10-11; 111pp; English.

XX The present sequence represents an interleukin (IL)-171 polypeptide.  
 CC It is a mammalian homologue of the cytokine designated CTLA-8 (also  
 CC referred to as IL-17). The specification also describes homologues  
 CC IL-171, IL-175, IL-172, IL-173, IL-174, IL-176, and IL-177. The DNA  
 CC sequence encoding IL-171 is useful for identifying genes, mRNA and  
 CC cDNA molecules which code for related or homologous proteins. The  
 CC IL-171 protein, antibodies against IL-171, and compounds which have  
 CC binding affinity to IL-171 are useful in treatment of conditions  
 CC associated with abnormal physiology or development, including abnormal  
 CC proliferation, e.g. cancerous conditions, or degenerative conditions.  
 CC The IL-171 protein can be used in kits and assay methods for identifying  
 CC compounds that selectively bind to IL-171.

XX Sequence 197 AA;

Query Match 100.0%; Score 1073; DB 21; Length 197;

Best Local Similarity 100.0%; Pred. No. 4.6e-109;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MTLIPGLLFTWLHTCLAHNDPSLRGHPHSHGTPHCYSAEELPLGAPPHLLARGAKMGQ 60

Db |||||  
 1 mtlipglflftwhtclahndpslrghphshgtpchysaeelpgqaphllargakwqg 60  
 Oy 61 ALPVALVSSLEAASHRGHREPSATTOCPVLRPEEVLADTHQRSTSPRYRVDTDEDY 120  
 |||||  
 Db 61 alpvalvssleaashrghrerpsattpcvlrrpeevleadthqrsisprryrvdtedy 120  
 Oy 121 POKLAFECICRCIDARTGRETAAALNSVRLQSLVLRRRPCSRDQSGLPFGAPAFHT 180  
 |||||  
 Db 121 pklafaeclctgcidartgretaaalnsrvllgslvlrrpcsrqsglprpgafafht 180  
 Oy 181 EFHVPVGCCTVLP RSV 197  
 |||||  
 Db 181 efihvpqctcvlprsv 197

## RESULT 4

AA92238  
 ID AAY92238 standard; Protein: 197 AA.

AC AAY92238;  
 DT 10-AUG-2000 (first entry)

DE Human interleukin-17 (IL-17) homologue.

KW Interleukin 17; IL-17; haematopoiesis; chemotherapy; cytostatic;  
 antianemic; cardiant; hemostatic; anti-inflammatory; anti-HIV.

OS Homo sapiens.

FT Key Location/Qualifiers  
 Peptide 1..18

FT Protein /label= signal\_peptide  
 19..197  
 FT /label= mature\_protein

PN WO200020593-A1.

PD 13-APR-2000.

PE 30-SEP-1999; 99WO-US22678.

PR 02-OCT-1998; 98US-0102883.

PR 01-DEC-1998; 98US-0110405.

PR 11-JUN-1999; 99US-0138910.

XX (ELIL ) LILLY & CO ERI.

PI Glasebrook AL, Su EW, Wei J, Liu L;

DR WPI: 2000-303778/26.  
 N-PSDB: AAA09153.

PT Nucleic acid encoding an interleukin-17 (IL-17) homolog polypeptide  
 PT which enhances hematopoiesis, useful for treating e.g. anemia,  
 PT thrombocytopenia, viral and bacterial infections

PS Claim 16; Page 92-93; 111pp; English.

XX Interleukin 17 (IL-17) stimulates hematopoiesis and production of  
 CC neutrophils, granulocytes, or platelets, this may be useful during  
 CC chemotherapy. IL-17 homologues have at least one activity selected  
 CC from induction of cytotoxic T cells, induction of lymphokine-activated  
 CC killer cell proliferation or a B or T cell stimulation. The IL-17  
 CC homologue may also be used to treat viral or bacterial infections.  
 CC immune related diseases, anemia, leukemia, thrombocytopenia, uremia,  
 CC Von Willebrand disease, postoperative cardiovascular dysfunction,  
 CC treatment of AIDS (acquired immune deficiency syndrome)-related bone  
 CC marrow failure, and inflammatory diseases of the gastrointestinal  
 CC system, joints, and lungs.

XX Sequence 197 AA;

Query Match 100.0%; Score 1073; DB 21; Length 197;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-109;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLPGLLFTWLHTCLAHNDPSLRGPHSHGTPHCYSABELPLGQAPPHILARGAKWGQ 60  
 Db 1 mtlpgllftlwlhtclahndpslrghshgtpchysaeelpgqapphilargakwgq 60

QY 61 ALPALVSSLEAASHRGHERPSATTOCPVLRPEVLEADTHORSISPMWRYVDDEDRY 120  
 Db 61 alpavlsleaashrgherpsatlcgvlrpeeveadthgrsispmwryvdtde dry 120

QY 121 POKLAFECRCRCIDARTGRETAALNSVRLQSLVLRRRPCSRDGSGLPTPGAFAFHT 180  
 Db 121 pklafaecrcrcidartgretaalnsvrlqslvlrrrrpcsrdsqglptpgafafht 180

QY 181 EFHVPVGCCTCVLPFRSV 197  
 Db 181 efhvpvgctcvlprsv 197

RESULT 5  
 AAY44460  
 ID AAY44460 standard; Protein; 197 AA.  
 XX AAY44460;  
 AC  
 XX  
 DT 27-MAR-2000 (first entry)  
 XX  
 DE Human Interleukin 17C, PRO1122 polypeptide.  
 XX  
 KW Interleukin; IL-17C; PRO1122 polypeptide; clone DNA62377-1381-1; UN0561;  
 KW cytokine IL-17; cytotoxic T-lymphocyte-associated antigen 8; CTLA-8;  
 KW hybridisation probe; antagonist; degenerative cartilaginous disorder;  
 KW agonist; diagnose; therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..18  
 FT /label= Signal\_Peptide  
 FT 19..197  
 FT /label= Mature\_IL-17C\_polypeptide  
 FT /note= "Used to treat degenerative cartilaginous disorder"  
 FT Misc-difference 109  
 FT /note= "Conserved Trp residue"  
 FT Misc-difference 129  
 FT /note= "Conserved Cys residue"  
 FT Misc-difference 134  
 FT /note= "Conserved Cys residue"  
 FT Misc-difference 163  
 FT /note= "Conserved Cys residue"  
 FT Misc-difference 189  
 FT /note= "Conserved Cys residue"  
 FT Misc-difference 191  
 FT /note= "Conserved Cys residue"  
 FT /note= "Conserved Cys residue"  
 XX  
 PN W0960127-A2.  
 XX  
 PD 25-NOV-1999.  
 XX  
 PF 14-MAY-1999; 99MO-US10733.  
 XX  
 PR 15-MAY-1998; 98US-0085579.  
 PR 23-DEC-1998; 98US-0113621.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Chen J, Flivaroff E, Goddard A, Gurney AL, Li H, Wood WI.  
 XX

DR WPI: 2000-116314/10.  
 DR N-PSDB; AAZ29728.  
 XX  
 FT New polypeptides designated PRO1031 and PRO1122 used to treat a  
 PT degenerative cartilaginous disorder -  
 XX  
 PS Claim 23; Fig 3; 141pp; English.  
 XX  
 CC The present sequence is the human PRO1122 polypeptide, also referred to  
 CC as UN0561, and as Interleukin-17C (IL-17C), encoded by  
 CC clone DNA62377-1381-1. This sequence has identity with the  
 CC cytokine IL-17 and cytotoxic T-lymphocyte-associated antigen 8 (CTLA-8)  
 CC and has leucine zipper pattern. PRO1122 is expressed in pancreas, small  
 CC intestine, stomach and testis also. It shares about 26-28% amino acid  
 CC identity with IL-17 and IL-17B. The entire coding region of IL-17C can  
 CC be used as hybridisation probe. The PRO1122 polypeptide, agonist or  
 CC antagonist, is used to diagnose and treat a degenerative cartilaginous  
 CC disorder.  
 XX  
 SQ Sequence 197 AA;

Query Match 100.0%; Score 1073; DB 21; Length 197;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-109;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLPGLLFTWLHTCLAHNDPSLRGPHSHGTPHCYSABELPLGQAPPHILARGAKWGQ 60  
 Db 1 mtlpgllftlwlhtclahndpslrghshgtpchysaeelpgqapphilargakwgq 60

QY 61 ALPALVSSLEAASHRGHERPSATTOCPVLRPEVLEADTHORSISPMWRYVDDEDRY 120  
 Db 61 alpavlsleaashrgherpsatlcgvlrpeeveadthgrsispmwryvdtde dry 120

QY 121 POKLAFECRCRCIDARTGRETAALNSVRLQSLVLRRRPCSRDGSGLPTPGAFAFHT 180  
 Db 121 pklafaecrcrcidartgretaalnsvrlqslvlrrrrpcsrdsqglptpgafafht 180

QY 181 EFHVPVGCCTCVLPFRSV 197  
 Db 181 efhvpvgctcvlprsv 197

RESULT 6  
 AAY53892  
 ID AAY53892 standard; Protein; 197 AA.  
 XX AAY53892;  
 AC  
 XX  
 DT 13-MAR-2000 (first entry)  
 XX  
 DE Amino acid sequence of human interleukin-21.  
 XX  
 KW Human; interleukin-22; IL-22; IL-21; immune system disorder;  
 KW immune cell chemotaxis; haematopoietic cell disorder;  
 KW haemostatic activity; thrombolytic activity; autoimmune disorder; asthma;  
 KW respiratory problem; organ rejection; graft-versus-host disease; GVHD;  
 KW inflammation; hyperproliferative disorder; tissue regeneration;  
 KW embryonic stem cell differentiation; embryonic stem cell proliferation;  
 KW haematopoietic lineage; allergic asthma.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..18  
 FT /note= "signal peptide"  
 FT 34..40  
 FT /note= "conserved domain V"  
 FT 63..68  
 FT /note= "conserved domain VI"  
 FT 104..109  
 FT /note= "conserved domain VII"  
 FT 113..121  
 FT Domain



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FT      Domain      /note="conserved domain I"
FT      129..134
FT      /note="conserved domain II"
FT      156..162
FT      Domain      /note="conserved domain III"
FT      185..192
FT      Domain      /note="conserved domain IV"
FT      WO9961617-A1.
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XX      02-DEC-1999.
XX
XX      27-MAY-1999; 99WO-US11644.
XX
XX      29-MAY-1998; 98US-0087340.
XX      10-SEP-1998; 98US-0099805.
XX      30-APR-1999; 99US-0131965.
XX
XX      (HUMA-) HUMAN GENOME SCI INC.
XX
XX      Ruben SM, Ebner R;
XX
XX      WPI: 2000-072622/06.
XX      N-PSDB: AA36836.
XX
XX      Novel polynucleotides used to develop products for treating e.g. immune
XX      disorders, blood disorders, autoimmune disorders, allergies,
XX      inflammation, hyperproliferative disorders or infections
XX
XX      Claim 26; Fig 6A-B; 170pp; English.
XX
XX      The present sequence represents a human interleukin-21 (IL-21)
XX      protein. The specification also describes IL-22 polynucleotides and
XX      polypeptides. The IL-21 polynucleotide was isolated from a cDNA library
XX      of apoptotic T-cells. IL-21 and IL-22 may be useful in treating
XX      deficiencies or disorders of the immune system, by activating or
XX      inhibiting the proliferation, differentiation, or mobilization
XX      (chemotaxis) of immune cells, treating or detecting deficiencies or
XX      disorders of haematopoietic cells, to modulate haemostatic or
XX      thrombolytic activity, in treating or detecting autoimmune disorders,
XX      treating asthma (particularly allergic asthma) or other respiratory
XX      problems, to treat and/or prevent organ rejection or graft-versus-host
XX      disease (GVHD), to modulate inflammation, to treat or detect
XX      hyperproliferative disorders, to treat or detect infectious agents, to
XX      differentiate, proliferate and attract cells, leading to the
XX      regeneration of tissues. IL-21 and IL-22 may also increase or decrease
XX      the differentiation or proliferation of embryonic stem cells and
XX      haematopoietic lineage, may be used to modulate mammalian
XX      characteristics.
XX
XX      Sequence 197 AA:
XX

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Query Match      100.0%; Score 1073; DB 21; Length 197;
Best Local Similarity 100.0%; Pred. No. 4.6e-109;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY      1 MNTLLPGLLTMTMLCLAHHDPSLRGHPHSHGTPHCYSAEELPLGAPPHLLARGAQWQ 60
DB      1 mltllpgliltwltlclahhdpslrghphshgtpchysaeelp1gqapphllarqakwq 60
OY      61 ALPVALVSSLEAASHRGHRSRPSATQCPVLRPEEVLADTHORSISPMRYRVDTDEDRY 120
DB      61 alpvalvssleaaashrghrsrpsatqcpvlrpeevleadtthorsispmryrvdtdedry 120
OY      121 POKLAFBECLRCGCDIARTGRETALNSVRLQSLILVLRPPCSRDGSLPTPGAFAFHT 180
DB      121 pqklafeaelrcgcidartgretalnsvrlqslilvlrrppcsrdgsllptpgafafht 180
OY      181 EFTHVPVGCVCVPRSV 197
DB      181 efthvpvgccvcvprsv 197

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RESULT 7
ID      AAG66121 standard; Protein; 197 AA.
XX
XX      AAG66121;
XX
XX      13-MAR-2002 (first entry)
XX
XX      Human Interleukin (IL)-21 amino acid sequence.
XX
XX      Interleukin; IL-21; IL-22; immunosuppressive; cytostatic; thrombolytic;
XX      antiinflammatory; antibacterial; gene therapy; human.
XX
XX      Homo sapiens.
XX
XX      Key      Location/Qualifiers
XX      Peptide 1..18
XX      Protein /note="signal peptide"
XX      19..197
XX      Domain /note="mature protein"
XX      34..40 "conserved domain V"
XX      63..68 "conserved domain VI"
XX      104..109 "conserved domain VII"
XX      113..121 "conserved domain VIII"
XX      /note="conserved domain I"
XX      129..134 "conserved domain II"
XX      156..162 "conserved domain III"
XX      185..192 "conserved domain IV"
XX      /note="conserved domain IV"
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XX      US2001023070-A1.
XX
XX      20-SEP-2001.
XX
XX      08-DEC-2000; 2000US-0731816.
XX
XX      29-MAY-1998; 98US-087340P.
XX      30-APR-1999; 99US-131965P.
XX      09-DEC-1999; 99US-169837P.
XX      27-MAY-1999; 99US-0320713.
XX      27-MAY-1999; 99WO-US11644.
XX
XX      (EBNE/) EBNER R.
XX      (RUBE/) RUBEN S M.
XX
XX      Ebner R, Ruben SM;
XX
XX      WPI: 2001-638470/73.
XX      N-PSDB: AA167878.
XX
XX      New interleukin-21 and interleukin-22 polynucleotides and polypeptides,
XX      useful for treating, preventing or diagnosing e.g. disorders of
XX      hematopoietic cells, autoimmune disorders, or hyperproliferative
XX      diseases
XX
XX      Claim 26; Fig 6A-B; 87pp; English.
XX
XX      The invention relates to novel human proteins designated interleukin
XX      (IL)-21 and IL-22. The IL-21 and IL-22 polynucleotides can be used in
XX      linkage analysis as a marker for those specific chromosome, in chromosome
XX      mapping, to control gene expression through triple helix formation or
XX      antisense DNA or RNA, in gene therapy, in identifying individuals from
XX      minute biological samples, as an alternative to restriction fragment
XX      length polymorphism (RFLP) analysis, as polymorphic markers for forensic
XX      purposes, as molecular weight markers, or as diagnostic probes. IL-21 and
XX      IL-22 polypeptides can be used to treat, prevent or diagnose diseases of
XX      the immune system by activating or inhibiting the proliferation,

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CC differentiation or mobilization of immune cells, disorders of  
 CC hematopoietic cells (e.g. leukaemia, human immunodeficiency virus (HIV)  
 CC infection, anemia, thrombocytopenia), autoimmune disorders (e.g. Grave's  
 CC disease, systemic lupus erythematosus, ophthalmia), graft versus host  
 CC disease, inflammation, hyperproliferative disorders, or infectious  
 CC diseases. The polypeptides are useful for generating antibodies, which  
 CC can be used to treat, inhibit or prevent diseases or conditions  
 CC associated with aberrant expression and/or activity of IL-21 or IL-22.  
 CC The present sequence represents the amino acid sequence of human IL-21.  
 CC  
 XX Sequence 197 AA:

Query Match 100.0%; Score 1073; DB 22; Length 197;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-109;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTLPLGLFLTWLHTCLAHNDPSLRGHPHSHTGPHCYSAEELPLGQAPPHLLARAKAWGQ 60  
 DB 1 mtlplglflftwhtclahndpslrghpshtgphcyseeelpigqapphllargakwqg 60  
 OY 61 ALPALVSSLEAASHRGHERPSATTQCPLYRPEEVLADTHORSISPMRYVDDEDY 120  
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 DB 121 pqklafaeclrcgidartgreetaalnsvrlqslvlrrppcsrdsgslpfgafafht 180  
 OY 181 EFHVPVGCCTVLPKRV 197  
 DB 181 efhvpvgctcvlpkrsv 197  
 RESULT 8  
 AAU29247  
 ID AAU29247 standard; Protein; 197 AA.  
 AC AAU29247;  
 XX 18-DEC-2001 (first entry)  
 DT  
 XX Human PRO polypeptide sequence #224.  
 DE  
 XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;  
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
 KM blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
 KM adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.  
 XX Homo sapiens.  
 OS  
 PN WO200168848-A2.  
 PD 20-SEP-2001.  
 XX  
 PF 28-FEB-2001; 2001MO-US06520.  
 XX  
 PR 01-MAR-2000; 2000MO-US05601.  
 PR 02-MAR-2000; 2000MO-US05841.  
 PR 03-MAR-2000; 2000US-187202P.  
 PR 06-MAR-2000; 2000US-186968P.  
 PR 14-MAR-2000; 2000US-189320P.  
 PR 14-MAR-2000; 2000US-189328P.  
 PR 15-MAR-2000; 2000MO-US06884.  
 PR 21-MAR-2000; 2000US-190828P.  
 PR 21-MAR-2000; 2000US-191007P.  
 PR 21-MAR-2000; 2000US-191048P.  
 PR 21-MAR-2000; 2000US-191314P.  
 PR 28-MAR-2000; 2000US-192655P.  
 PR 29-MAR-2000; 2000US-193032P.  
 PR 30-MAR-2000; 2000MO-US08439.  
 PR 04-APR-2000; 2000US-194449P.

PR 04-APR-2000; 2000US-194647P.  
 PR 11-APR-2000; 2000US-195975P.  
 PR 11-APR-2000; 2000US-196000P.  
 PR 11-APR-2000; 2000US-196187P.  
 PR 11-APR-2000; 2000US-196690P.  
 PR 11-APR-2000; 2000US-196820P.  
 PR 18-APR-2000; 2000US-198121P.  
 PR 18-APR-2000; 2000US-198585P.  
 PR 25-APR-2000; 2000US-199397P.  
 PR 25-APR-2000; 2000US-199550P.  
 PR 25-APR-2000; 2000US-199654P.  
 PR 03-MAY-2000; 2000MO-US13705.  
 PR 17-MAY-2000; 2000MO-US13705.  
 PR 22-MAY-2000; 2000MO-US14042.  
 PR 30-MAY-2000; 2000MO-US14941.  
 PR 02-JUN-2000; 2000MO-US15264.  
 PR 05-JUN-2000; 2000US-209832P.  
 PR 28-JUL-2000; 2000MO-US20710.  
 PR 22-AUG-2000; 2000US-0644848.  
 PR 24-AUG-2000; 2000MO-US23328.  
 PR 08-NOV-2000; 2000MO-US30952.  
 PR 01-DEC-2000; 2000MO-US32678.  
 PR 20-DEC-2000; 2000MO-US34956.

PA (GENTH) GENENTECH INC.

PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
 PI Pan J, Smith V, Watanabe CK, Wood MT, Zhang Z;

DR WPI: 2001-602746/68.  
 DR N-PSDB; AAS46148.

PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
 PT presence of tumours, such as prostate and breast tumours, in mammals and  
 PT to screen for modulators of the compounds

XX Claim 11; Fig 448; 774pp; English.

XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.  
 CC The PRO polypeptides and their associated nucleic acids can be used to  
 CC detect the presence of a tumour in a mammal by comparing the level of  
 CC expression of a PRO polypeptide in a test sample of cells from the animal  
 CC and a control sample of normal cells, whereby a higher level of  
 CC expression in the test sample indicates the presence of a tumour in the  
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, goats  
 CC and rabbits but are preferably human. The polypeptides can be used to  
 CC stimulate tumour necrosis factor (TNF) alpha release from human blood,  
 CC when contacted with it. A specific polypeptide can be used to stimulate  
 CC the proliferation or differentiation of chondrocyte cells. The PRO  
 CC proteins can be used to determine the presence of tumours and also  
 CC susceptibility to tumour development, particularly adrenal, lung, colon,  
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
 CC can be used for genetic analysis of individuals with genetic disorders.  
 XX

SQ Sequence 197 AA:

Query Match 100.0%; Score 1073; DB 22; Length 197;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-109;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTLPLGLFLTWLHTCLAHNDPSLRGHPHSHTGPHCYSAEELPLGQAPPHLLARAKAWGQ 60  
 DB 1 mtlplglflftwhtclahndpslrghpshtgphcyseeelpigqapphllargakwqg 60  
 OY 61 ALPALVSSLEAASHRGHERPSATTQCPLYRPEEVLADTHORSISPMRYVDDEDY 120  
 DB 61 alpavlsleaashrgtherpsattqcpvlyrpeeveleadthgrtsispmryvdedy 120  
 OY 121 POKLAFAECLRCGIDARGRETAALNSVRLQSLVLRPPCRSDGSGLPFGAFAPHT 180  
 DB 121 pqklafaeclrcgidartgreetaalnsvrlqslvlrrppcsrdsgslpfgafafht 180

OY 181 EFHVPVGTCTVLPVRSV 197  
 |||||||  
 DB 181 efhvpvgctcvlprsv 197

## RESULT 9

AAU04951

AAU04951 standard; Protein; 197 AA.

AC AAU04951;

24-OCT-2001 (first entry)

Human Interleukin 17C ligand, IL-17C.

Human; Interleukin-17C ligand; IL-17C; agonist; antagonist;

rheumatoid arthritis; systemic lupus erythematosus;

allergic disease; asthma; demyelinating disease;

degenerative cartilaginous disorder; transplantation associated disease.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 1..18 /label= Signal\_peptide

FT Region 3..25 /note= "Leucine zipper pattern"

FT Protein 19..197 /label= Mature\_IL\_17C

FT Region 32..38 /note= "N-myristoylation site"

FT Region 55..61 /note= "N-myristoylation site"

FT Region 99..125 /note= "Region homologous to IL-17"

FT Region 112..121 /note= "Tyrosine kinase phosphorylation site"

FT Region 133..139 /note= "N-myristoylation site"

XX WO20016420-A2.

XX 28-JUN-2001.

XX 20-DEC-2000; 2000WO-US34956.

XX 23-DEC-1999; 99US-0172096.

XX 30-DEC-1999; 99WO-US31274.

XX 11-JAN-2000; 2000US-0175481.

XX 18-FEB-2000; 2000WO-US04341.

XX 02-MAR-2000; 2000WO-US05841.

XX 21-MAR-2000; 2000US-0191007.

XX 02-JUN-2000; 2000WO-US07532.

XX 22-JUN-2000; 2000US-0213087.

XX 22-AUG-2000; 2000US-0644848.

XX 24-AUG-2000; 2000WO-US23328.

XX 24-OCT-2000; 2000US-0242837.

XX 10-NOV-2000; 2000WO-US30873.

XX 28-NOV-2000; 2000US-0253646.

XX 01-DEC-2000; 2000WO-US32678.

XX (GETH ) GENENTECH INC.

XX Chen J, Filvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi CJ;

XX Gurney AL, Li H, Hillan KJ, Tumas D, Van Lookeren M, Vandalen RL;

XX Watanabe CK, Williams PM, Wood WL, Yansura DG;

XX WPI; 2001-451708/48.

XX N-PSDB; AAS09510.

PT Novel PRO polypeptides homologous to interleukin-17, useful for the  
 PT diagnosis and treatment of immune related disease e.g. rheumatoid  
 PT arthritis and diabetes

PS Claim 10; Fig 4; 18pp; English.

XX The sequence is PRO1122 which is the human interleukin 17C ligand,  
 CC IL-17C, encoded by DNA 62377-1381-1. A composition  
 CC containing antagonists to the PRO polypeptides or individual components  
 CC are useful for treating a mammal with an immune related disease, e.g.  
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, an  
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an  
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal  
 CC disease, a demyelinating disease, an autoimmune or immune-mediated skin  
 CC disease, contact dermatitis, an allergic disease e.g. food  
 CC hypersensitivity, asthma, a transplantation associated disease, or a  
 CC chronic inflammatory demyelinating polyneuropathy. Treating a  
 CC degenerative cartilaginous disorder comprises administering a PRO1031 or  
 CC PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous  
 CC examples of the diseases and disorders are given in the specification.

SQ Sequence 197 AA;

Query Match 100.0%; Score 1073; DB 22; Length 197;  
 Best Local Similarity 100.0%; Pred No. 4.6e-109;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTLPLLELTWLTCLAHNDPSLRGPHSHGTPHCYSAEELPLGAPHLARGAKWQ 60

DB 1 mtlplllflftwhtclahndpslrghshgtpchysaeelplgqpphllargakwq 60

OY 61 ALPVAVSSLEASHGRHSPSATTCQVLPREEVLEADTHQRSISPMARYDTEDEK 120

DB 61 alpvalvssleaashgrhspattpcqlrpeevleadthqrsispmaryrvtdeky 120

OY 121 POKLAFACRCRCIDARCFERFALNSVRLQSLVLRPPSRGSGPFGARAFH 180

DB 121 pqlafacrcrcidarcfertaalnsvrlqslvlrrppsrsgslpfgatafnt 180

OY 181 EFHVPVGTCTVLPVRSV 197

DB 181 efhvpvgctcvlprsv 197

## RESULT 10

AAAY44485

AAAY44485 standard; Protein; 206 AA.

XX AAAY44485;

XX 27-MAR-2000 (first entry)

XX Human Interleukin 17C with C-terminal Gly(His)8 tag, IL-17C.his.

XX Interleukin; IL-17C.his; PRO1122 polypeptide; clone DNA62377-1381-1;

XX immunoprecipitation; IL-17 receptor extracellular domain; IL-17R ECD;

XX cytokine IL-17; hybridisation probe; antagonist; Gly(His)8 tag; agonist;

XX degenerative cartilaginous disorder; diagnosis; therapy.

XX Homo sapiens.

XX (GETH ) GENENTECH INC.

XX Chen J, Filvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi CJ;

XX Gurney AL, Li H, Hillan KJ, Tumas D, Van Lookeren M, Vandalen RL;

XX Watanabe CK, Williams PM, Wood WL, Yansura DG;

XX WPI; 2001-451708/48.

XX N-PSDB; AAS09510.

FT Misc-difference 129 /note="Conserved Cys residue"  
 FT Misc-difference 134 /note="Conserved Cys residue"  
 FT Misc-difference 163 /note="Conserved Cys residue"  
 FT Misc-difference 189 /note="Conserved Cys residue"  
 FT Misc-difference 191 /note="Conserved Cys residue"  
 FT Misc-difference 198.206 /note="Conserved Cys residue"  
 FT Misc-difference 198.206 /note="C-terminal Gly(His)8 tag"  
 XX  
 XX W09960127-A2.  
 XX  
 XX 25-NOV-1999.  
 XX  
 XX 14-MAY-1999; 99WO-US10733.  
 XX  
 XX 15-MAY-1998; 98US-0085579.  
 XX 23-DEC-1998; 98US-0113621.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 XX Chen J, Filvaroff E, Goddard A, Gurney AL, Li H, Wood WI;  
 XX WPI; 2000-116314/10.  
 XX  
 XX New polypeptides designated PRO1031 and PRO1122 used to treat a  
 XX degenerative cartilaginous disorder -  
 XX  
 XX Example 11; Page 138-139; 141pp; English.  
 XX  
 XX The present sequence is the human PRO1122 polypeptide, with a C-terminal  
 XX Gly(His)8 tag, IL-17C, his, derived from the clone DNA62377-1381-1.  
 XX This sequence is used in a competitive binding experiment for the  
 XX immunoprecipitation of IL-17 receptor extracellular domain (IL-17R ECD).  
 XX The entire coding region of IL-17C can be used as hybridisation probe.  
 XX The PRO1122 polypeptide, agonist or antagonist, is used to diagnose and  
 XX treat a degenerative cartilaginous disorder.  
 XX  
 XX Sequence 206 AA;

Query Match 100.0%; Score 1073; DB 21; Length 206;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-109;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLPGILFLTWLHTCLAHNDPSLRGPHSHGTPHCYSAEELPLGQAPPHILARGAQWQ 60  
 DB 1 MTLPGILFLTWLHTCLAHNDPSLRGPHSHGTPHCYSAEELPLGQAPPHILARGAQWQ 60  
 QY 61 ALPALVSSLEAASHRGHRRPSATQCPLYRPEEVLADPHORSISPMRYRVDTEDRY 120  
 DB 61 ALPALVSSLEAASHRGHRRPSATQCPLYRPEEVLADPHORSISPMRYRVDTEDRY 120  
 QY 121 POKIAFAECLRCGICDARTGRETALNSVRLLOSILVLRRRPCSDGSLPTPGAFAPFT 180  
 DB 121 POKIAFAECLRCGICDARTGRETALNSVRLLOSILVLRRRPCSDGSLPTPGAFAPFT 180  
 QY 181 EFLHVPVGCVCVLPKRSV 197  
 DB 181 EFLHVPVGCVCVLPKRSV 197

RESULT 11  
 AAY44462  
 ID AAY44462 standard; Protein; 425 AA.

XX AAY44462;  
 XX 27-MAR-2000 (first entry);  
 XX

DE Human Interleukin 17C-19G1 FC fusion protein, hIL-17C.fc.  
 XX Interleukin; IL-17C.fc: fusion protein; PRO1122 polypeptide; cytokine;  
 XX human IgG1; fluorescence-activated cell sorter analysis; FACS;  
 XX Tumour Necrosis Factor-alpha; TNF-alpha; leukemic monocyte; THP-1 cell.  
 XX Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 XX Peptide 1..18  
 XX Protein /label= signal\_peptide  
 XX 19..197  
 XX /label= Mature IL-17C polypeptide  
 XX /note= "Used to treat degenerative cartilaginous  
 XX disorder"  
 FT Misc-difference 109 /note="Conserved Trp residue"  
 FT Misc-difference 129 /note="Conserved Cys residue"  
 FT Misc-difference 134 /note="Conserved Cys residue"  
 FT Misc-difference 163 /note="Conserved Cys residue"  
 FT Misc-difference 189 /note="Conserved Cys residue"  
 FT Misc-difference 189 /note="Conserved Cys residue"  
 FT Misc-difference 191 /note="Conserved Cys residue"  
 FT Misc-difference 191 /note="Conserved Cys residue"  
 FT Region /note="Conserved Cys residue"  
 FT 197..425  
 FT /note="Sequence derived from FC region of human, IgG1"  
 XX  
 XX W09960127-A2.  
 XX  
 XX 25-NOV-1999.  
 XX  
 XX 14-MAY-1999; 99WO-US10733.  
 XX  
 XX 15-MAY-1998; 98US-0085579.  
 XX 23-DEC-1998; 98US-0113621.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 XX Chen J, Filvaroff E, Goddard A, Gurney AL, Li H, Wood WI;  
 XX WPI; 2000-116314/10.  
 XX  
 XX New polypeptides designated PRO1031 and PRO1122 used to treat a  
 XX degenerative cartilaginous disorder -  
 XX  
 XX Example 12; Page 129-130; 141pp; English.

The present sequence is the human IL-17C.fc fusion protein, derived from  
 CC PRO1122 polypeptide and the FC region of human IgG1. The cytokine IL-17C  
 CC can be used to induce the release of TNF-alpha from human leukemic  
 CC monocytic, THP-1 cells. The fusion protein, IL-17C.fc is used to identify  
 CC the binding of IL-17C to THP-1 cells, using fluorescence-activated cell  
 CC sorter analysis (FACS).  
 XX  
 XX Sequence 425 AA;

Query Match 100.0%; Score 1073; DB 21; Length 425;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-108;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLPGILFLTWLHTCLAHNDPSLRGPHSHGTPHCYSAEELPLGQAPPHILARGAQWQ 60  
 DB 1 MTLPGILFLTWLHTCLAHNDPSLRGPHSHGTPHCYSAEELPLGQAPPHILARGAQWQ 60  
 QY 61 ALPALVSSLEAASHRGHRRPSATQCPLYRPEEVLADPHORSISPMRYRVDTEDRY 120  
 DB 61 ALPALVSSLEAASHRGHRRPSATQCPLYRPEEVLADPHORSISPMRYRVDTEDRY 120  
 QY 121 POKIAFAECLRCGICDARTGRETALNSVRLLOSILVLRRRPCSDGSLPTPGAFAPFT 180

Db 121 pklafaeclrgcldartgretalaansvrlqslvlrrpcsrdsqslpqpafatht 180  
 OY 181 EFHVPVGTCTVLPKRSV 197  
 181 efthvpvgtctvlpkrsv 197

## RESULT 12

AAE08676 standard: Protein; 227 AA.

AC AAE08676;

DE 15-NOV-2001 (first entry)

Human Interleukin (IL)-17 like protein.

Human; Interleukin; IL-17 like protein; rheumatic disease; gene therapy;  
 multiple sclerosis; graft versus host disease; inflammatory disease;  
 asthma; autoimmune disease; allergy; graft rejection; bone destruction;  
 drug screening; antiinflammatory; immunosuppressive; antiasthmatic;  
 neuroprotective; antirheumatic; antiallergic.

Homo sapiens.

Key Location/Qualifiers

Peptide 5..48

Protein /label= Signal\_peptide  
 49..227  
 /label= Mature\_human\_IL-17\_like protein

WO200159120-A2.

16-AUG-2001.

07-FEB-2001; 2001WO-US03916.

08-FEB-2000; 2000US-0180864.

27-NOV-2000; 2000US-0722920.

(AMGE-) AMGEN INC.

Jing S, Bass MB;

WPI; 2001-529841/58.

N-PSDB; AAD15291..

Novel interleukin-17 like polypeptides and nucleic acid molecules  
 encoding them useful for diagnosis, prevention and treatment of  
 inflammatory, autoimmune disease, allergies, asthma and organ or graft  
 rejection

Claim 14; Fig 1A; 117pp; English.

The present invention relates to interleukin (IL)-17 like polypeptides  
 and nucleic acids encoding them. IL-17 like protein is useful for  
 identifying binding partners, agonists and antagonists which can be used  
 for treating one or more diseases or disorders and for cloning IL-17  
 like receptors, using an expression cloning strategy. Radiolabelled or  
 affinity/activity-tagged IL-17 proteins are useful in binding assays to  
 identify a cell type or cell line or tissue that express IL-17 like  
 receptors. A radiolabelled or tagged IL-17 like protein is useful as an  
 affinity ligand to identify and isolate from an expression library the  
 subset of cells which express the IL-17 like receptors on their surface.  
 IL-17 like protein, agonist and antagonist are useful for treating acute  
 and chronic inflammation such as rheumatic diseases, graft versus host  
 disease and multiple sclerosis. IL-17 like antagonists are useful for  
 treating and preventing inflammatory disease, autoimmune disease,  
 allergies, asthma and organ or graft rejection in a patient and also  
 for inhibiting T cell proliferation and/or activation, in vivo B cell  
 proliferation or immunoglobulin secretion, and for blocking the effects  
 of IL-17 in inducing bone destruction. IL-17 like molecule is useful in

CC gene therapy and for mapping the location of the IL-17 like gene and  
 CC related genes on chromosomes, as hybridisation probes in diagnostic  
 CC assays. Non-human animals in which the promoter for one or more of IL-17  
 CC like protein is either activated or inactivated are useful for drug  
 CC candidate screening. The present sequence is human IL-17 like protein.  
 CC  
 SQ Sequence 227 AA;

Query Match 99.1%; Score 1063; DB 22; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-108;  
 Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 ILPGILFLTWLHTCLAHNPSSLRGHPHSGTTPHCYSAEELPLGQAPPHLLARGAKKGOAL 62  
 Db 33 ILPGILFLTWLHTCLAHNPSSLRGHPHSGTTPHCYSAEELPLGQAPPHLLARGAKKGOAL 92  
 OY 63 PVALLVSSLEAASHRHGRHRSATTCQPVLRPEEVLADTHQRSISPMRYRVDTEDRYQ 122  
 Db 93 PVALLVSSLEAASHRHGRHRSATTCQPVLRPEEVLADTHQRSISPMRYRVDTEDRYQ 152  
 OY 123 KLAFACLCRGCTDARTGRETALNSVRLQSLVLRRRPCSDSGGLPFGAFATHTF 182  
 Db 153 KLAFACLCRGCTDARTGRETALNSVRLQSLVLRRRPCSDSGGLPFGAFATHTF 212  
 OY 183 IHVPVGTCTVLPKRSV 197  
 Db 213 IHVPVGTCTVLPKRSV 227

## RESULT 13

AAE08680 standard: Protein; 227 AA.

AC AAE08680;

DE 15-NOV-2001 (first entry)

Human Interleukin (IL)-17 like protein mutant (Leu47Ile).

Human; Interleukin; IL-17 like protein; rheumatic disease; gene therapy;  
 multiple sclerosis; graft versus host disease; inflammatory disease;  
 asthma; autoimmune disease; allergy; graft rejection; bone destruction;  
 drug screening; antiinflammatory; immunosuppressive; antiasthmatic;  
 neuroprotective; antirheumatic; antiallergic; mutant; mutein.

Homo sapiens.

OS Synthetic.

Key Location/Qualifiers  
 Misc-difference 47 /note= "Wild-type Leu substituted with Ile"

WO200159120-A2.

16-AUG-2001.

07-FEB-2001; 2001WO-US03916.

08-FEB-2000; 2000US-0180864.

27-NOV-2000; 2000US-0722920.

(AMGE-) AMGEN INC.

Jing S, Bass MB;

WPI; 2001-529841/58.

Novel interleukin-17 like polypeptides and nucleic acid molecules  
 encoding them useful for diagnosis, prevention and treatment of  
 inflammatory, autoimmune disease, allergies, asthma and organ or graft  
 rejection

Claim 18; Page -; 117pp; English

PS Claim 18; Page -7; IL17pp; English.

XX  
PS  
CC The present invention relates to interleukin (IL)-17 like polypeptides  
CC and nucleic acids encoding them. IL-17 like protein is useful for  
CC identifying binding partners, agonists and antagonists which can be used  
CC for treating one or more diseases or disorders and for cloning IL-17  
CC like receptors, using an expression cloning strategy. Radiolabelled or  
CC affinity/actively-tagged IL-17 proteins are useful in binding assays to  
CC identify a cell type or cell line or tissue that express IL-17 like  
CC receptors. A radiolabelled or tagged IL-17 like protein is useful as an  
CC affinity ligand to identify and isolate from an expression library the  
CC subset of cells which express the IL-17 like receptors on their surface.  
CC IL-17 like protein, agonist and antagonist are useful for treating acute  
CC and chronic inflammation such as rheumatic diseases, graft versus host  
CC disease and multiple sclerosis. IL-17 like antagonists are useful for  
CC treating and preventing inflammatory disease, autoimmune disease,  
CC allergies, asthma and organ or graft rejection in a patient and also  
CC for inhibiting T cell proliferation and/or activation, in vivo B cell  
CC proliferation or immunoglobulin secretion, and for blocking the effects  
CC of IL-17 in inducing bone destruction. IL-17 like molecule is useful in  
CC gene therapy and for mapping the location of the IL-17 like gene and  
CC related genes on chromosomes, as hybridisation probes in diagnostic  
CC assays. Non-human animals, in which the promoter for one or more of IL-17  
CC like protein is either activated or inactivated are useful for drug  
CC candidate screening. The present sequence is human IL-17 like  
CC candidate mutant (Leu47Ile).

CC Note: The present sequence is not shown in the specification, but is  
CC derived from the human IL-17 like protein referred to as SEQ ID NO:2  
CC (AAE08676), shown in figure 1A.

XX  
CC  
Sequence 227 AA:

SQ Sequence 227 AA;

Query Match	98.9%	Score 1061	DB 22	Length 227
Best Local Similarity	99.5%	Pred. No. 1.1e-107		
Matches 194	Conservative 1	Mismatches 0	Indels 0	Gaps 0
QY 3	LLLEGLLETLWLTCLAHNDPSLGRHPHSHGPHCYSAEELPLGQAPPHILARGAKMGQAL	62		
Db 33	LLPPLILFLTLVHLCIIRHGPSIRGPHSHGPHCYSAEELPLGQAPPHILARGAKMGQAL	92		
QY 63	PVALVSLSLAASRGHRRPSATTCQPVLRPEEVLEATHORSLSPWRIRYDITDEDRIPO	122		
Db 93	PVALVSLSLAASIRGHPSPATTCQPVLRPEEVLEATHORSLSPWYIVDTLEDITYPA	152		
QY 123	KLAFAECLRCGCDIARTGREGTAAALNSVRLLOSILVLRRRPSCSPGSGPLPPGCAAFPTFR	182		
Db 153	KLAFAECLRCGCDIARTGREGTAAALNSVRLLOSILVLRRRPSCSPGSGPLPPGCAAFPTFR	182		
QY 183	IHPVPGCTGLPRSV	197		
Db 213	IHPVPGCTGLPRSV	227		

RESULT	14
AAE08682	
ID	AAE08682 standard; Protein; 227 AA
RY	

AC AAE08682;

DT 15-NOV-2001 (first entry)

Human interleukin (IL)-17 like protein mutant (Leu47Met)

KW multiple sclerosis; graft versus host disease; inflammatory disease;  
 KW asthma; autoimmune disease; allergy; graft rejection; bone destruction;  
 KW drug screening; antiinflammatory; immunosuppressive; antiautomatic;  
 KW neuroprotective; antirheumatic; antiallergic; mutant; muten.

05	Homo sapiens
05	Synthetic.

FH	Key	Location/Qualifiers
FT	Misc-difference	47

FT	Misc-difference	47
FT	/note= "Wild-type Ieu substituted with Met"	
FT		
xx		

PN WO200159120-A2  
XX

PD 16-AUG-2001

PE : 07-FEB-2001; 2001WO-US03916.  
XX

PR 27-NOV-2000; 2000US-0722920.

PA (AMGE-) AMGEN INC.

PI Jing S, Bass MB;

DR WPL; 2001-529841/58  
XX

PT Novel interleukin-17 like polypeptides and nucleic acid molecules  
PT encoding them useful for diagnosis, prevention and treatment of  
PT inflammatory, autoimmune disease, allergies, asthma and organ or graft  
XX rejection -  
XX  
PS Claim 18, Page -, 117pp; English.  
XX

The present invention relates to interleukin (IL)-17 like polypeptides and nucleic acids encoding them. IL-17 like protein is useful for identifying binding partners, agonists and antagonists which can be used for treating one or more diseases or disorders and for cloning IL-17 like receptors, using an expression cloning strategy. Radiolabelled or affinity/actively-tagged IL-17 proteins are useful in binding assays to identify a cell type or cell line or tissue that expresses IL-17 like receptors. A radiolabelled or tagged IL-17 like protein is useful as an affinity ligand to identify and isolate from an expression library the subset of cells which express the IL-17 like receptors on their surface. IL-17 like protein, agonist and antagonist are useful for treating acute and chronic inflammation such as rheumatic diseases, graft versus host disease and multiple sclerosis. IL-17 like antagonists are useful for treating and preventing inflammatory disease, autoimmune disease, allergies, asthma and organ or graft rejection in a patient and also for inhibiting T cell proliferation and/or activation, in vivo B cell proliferation or immunoglobulin secretion, and for blocking the effects of IL-17 in inducing bone destruction. IL-17 like molecule is useful in gene therapy and for mapping the location of the IL-17 like gene and related genes on chromosomes, as hybridisation probes in diagnostic assays. Non-human animals in which the promoter for one or more of IL-17 like protein is either activated or inactivated are useful for drug candidate screening. The present sequence is human IL-17 like protein mutant (Leu47Met).

Note: The present sequence is not shown in the specification, but is derived from the human IL-17 like protein referred to as SEQ ID No.:2 (AAE08676), shown in figure 1A.

Sequence 227 AA

Query Match	98.9%	Score 1061:	DB 22:	Length 227:
Best Local Similarity	99.5%	Pred. No. 1	1e-107:	
Matches 194:	Conservative	0:	Indels	0:
			Gaps	0:

QY	3	LIIGLLELTWTVAHTGCAHHNDELRGHPHSHOTPHCYSAEELPLGQAPRPHLLAGAGWGAL	62
Db	33	LIPLGILFLTWHTCMAHDPRLGHPHSHYTPHCYSAEELPLGQAPRPHLLARGAGWGAL	92
QY	63	PVALVSSLEAASHRGHRHESPATQCVLRLPEVLEADHONSISPMWRVYTDDEDRPO	122
Db	93	PVALVSSLEAASHRGHRHESPATQCVLRLPEVLEADHONSISPMWRVYTDDEDRPO	155
QY	123	KLAFAECRCRCIDARTGRTETAAALNSVRLQSLVLRRRRCSRDSSGLPTPAFAFTHFF	182
Db	153	KIAFAECRCRCIDARTGRTETAAALNSVRLQSLVLRRRRCSRDSSGLPTPAFAFTHFF	213

Qy 183 IHVPVGTCTVLP RSV 197  
 Db 213 lhpvgctcvlprsv 227

## RESULT 15

AAE08681  
 ID AAE08681 standard; Protein; 227 AA.

XX AAE08681:

XX 15-NOV-2001 (first entry)

DE Human interleukin (IL)-17 like protein mutant (Leu47Val).

XX Human; interleukin; IL-17 like protein; rheumatic disease; gene therapy;  
 KW multiple sclerosis; graft versus host disease; inflammatory disease;  
 KW asthma; autoimmune disease; allergy; graft rejection; bone destruction;  
 KW drug screening; antiinflammatory; immunosuppressive; antiasthmatic;  
 KW neuroprotective; antirheumatic; antiallergic; mutant; mutein.

XX Homo sapiens.  
 OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 47 /note= "Wild-type Leu substituted with Val"

FT W0200159120-A2.

XX 16-AUG-2001.

XX 07-FEB-2001; 2001WO-US03916.

XX 08-FEB-2000; 2000US-0180864.

XX 27-NOV-2000; 2000US-0722920.

XX (AMGE-) AMGEN INC.

XX Jing S. Bass MB;

XX WPI; 2001-529841/58.

XX Novel interleukin-17 like polypeptides and nucleic acid molecules  
 PT encoding them useful for diagnosis, prevention and treatment of  
 PT inflammatory, autoimmune disease, allergies, asthma and organ or graft  
 PT rejection

XX Claim 18; Page -: 117pp; English.

XX The present invention relates to interleukin (IL)-17 like polypeptides  
 CC and nucleic acids encoding them. IL-17 like protein is useful for  
 CC identifying binding partners, agonists and antagonists which can be used  
 CC for treating one or more diseases or disorders and for cloning IL-17  
 CC like receptors, using an expression cloning strategy. Radiolabelled or  
 CC affinity/activity-tagged IL-17 proteins are useful in binding assays to  
 CC identify a cell type or cell line or tissue that express IL-17 like  
 CC receptors. A radiolabelled or tagged IL-17 like protein is useful as an  
 CC affinity ligand to identify and isolate from an expression library the  
 CC subset of cells which express the IL-17 like receptors on their surface.  
 CC IL-17 like protein, agonist and antagonist are useful for treating acute  
 CC and chronic inflammation such as rheumatic diseases, graft versus host  
 CC disease and multiple sclerosis. IL-17 like antagonists are useful for  
 CC treating and preventing inflammatory disease, autoimmune disease,  
 CC allergies, asthma and organ or graft rejection in a patient and also  
 CC for inhibiting T cell proliferation and/or activation, in vivo B cell  
 CC proliferation or immunoglobulin secretion, and for blocking the effects  
 CC of IL-17 in inducing bone destruction. IL-17 like molecule is useful in  
 CC gene therapy and for mapping the location of the IL-17 like gene and  
 CC related genes on chromosomes, as hybridisation probes in diagnostic  
 CC assays. Non-human animals in which the promoter for one or more of IL-17  
 CC like protein is either activated or inactivated are useful for drug  
 CC candidate screening. The present sequence is human IL-17 like

CC protein mutant (Leu47Val).  
 CC Note: The present sequence is not shown in the specification, but is  
 CC derived from the human IL-17 like protein referred to as SEQ ID NO:2  
 CC (AAE08676), shown in figure 1A.

XX SQ Sequence 227 AA;

Query Match 98.8%; Score 1060; DB 22; Length 227;  
 Best Local Similarity 99.5%; Pred. No. 1.5e-107;  
 Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ILPGILFTWLHTCLAHDPDLRGHPHSHGPHCYSAEELPLGQAPPHLLARGAKGQAL 62  
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 Db 93 pvalvssleashaargrherpsattqcpvlrpeeveadthqrsispwrvdtdedrypq 152  
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 Db 153 klafaecicrcgidartgretalnsvrlqslvlrrpcrdsgslpfgafphfhtef 212  
 Qy 183 IHVPVGTCTVLP RSV 197  
 Db 213 lhpvgctcvlprsv 227

Search completed: September 4, 2002, 01:57:15  
 Job time: 327 sec





GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 3, 2002, 23:54:32 ; Search time 1827.84 seconds  
(without alignments)  
11986.872 Million cell updates/sec

Title: US-09-854-280-4  
Perfect score: 1047  
Sequence: 1 gccaggtgtcagccgctc.....tgatgaacacatcccaaaa 1047

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues  
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: GenEmbl:\*  
2: gb\_ba:\*  
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4: gb\_in:\*  
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6: gb\_ov:\*  
7: gb\_pat:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sy:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htgo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No. Query Match Length DB ID Description

1	1047	100.0	1047	6	AX180766	AX180766 Sequence
2	1047	100.0	1047	9	AF152099	AF152099 Homo sapi
3	1015.4	97.0	1078	9	AF142410	AF142410 Homo sapi
4	923.4	88.2	1177	6	AX223849	AX223849 Sequence
5	651	62.2	15689	2	AC103884	AC103884 Homo sapi
6	651	62.2	157090	2	AC022554	AC022554 Homo sapi
7	192.8	18.4	221647	10	AL591003	AL591003 Mouse DNA
8	69.8	6.7	125020	9	AF429315	AF429315 Homo sapi
9	61	5.8	125020	9	AF429315	AF429315 Homo sapi
10	58.2	5.6	7218	6	I66494	I66494 Sequence 14
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12	53.8	5.1	486	9	AF458059	AF458059 Homo sapi
13	53.8	5.1	504	6	AX299773	AX299773 Sequence
14	53.8	5.1	644	6	AX253225	AX253225 Sequence
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18	53.6	5.1	204292	2	AP004071	AP004071 Oryza sat
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21	52.2	5.0	1320	6	AX092424	AX092424 Sequence
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28	50.2	4.8	135119	2	AC011578	AC011578 Homo sapi
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## ALIGNMENTS

RESULT 1  
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DEFINITION Sequence 3 from Patent WO0146420.  
ACCESSION AX180766  
VERSION AX180766.1 GI:15132617  
KEYWORDS  
SOURCE  
ORGANISM human.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

## REFERENCE

1 (bases 1 to 1047)  
Chen, J., Flyvareff, E., Fong, S., Goddard, A., Godowski, P. J.,  
Grimaldi, C. J., Gurney, A. L., Li, H., Hillan, K. J., Tumas, D., van  
Lookeren, M., Vandlen, R. L., Watanabe, C. K., Williams, P. M., Wood, W. I.,  
Il-17 and Il-17r homologous polypeptides and therapeutic uses  
thereof  
JOURNAL Patent, WO, 0146420-A 3 28-JUN-2001;  
Genentech, Inc. (US)  
FEATURES  
Location/Qualifiers  
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BASE COUNT 177 a 381 c 280 g 209 t  
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Matches 1047; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## RESULT 2

AF152099

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

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/chromosome="2"

/map="2q31"

/clone="DNA62377"

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/note="IL-17C; similar to Interleukin 17"

/codon\_start=1

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/protein\_id="AA628105.1"

/db\_xref="GI:6759915"

/translation="MTLLPGLPLTMTLTCIAHDPSPRGPHSHGTPHCYSAEPL

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QRSLSPWRYRVDTEDRYPQRIARAECLRCRIDARIGRETAALNSVLLLOSLVLR

RPSRDSGGLTPGAFARHTEFIHVPVCTCLPRSV"

BASE COUNT

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381 c

280 g

209 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 7.4e-207;  
Matches 1047; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 181 cggcagagcccccccaacactgctgctgagagtgcaagtgagggggagagagagagagag 240

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241	agccctgtgtcagacccctgagaggaagcaagccacaagggggagggagcaaggaagcctcaagc	human.	AF142410	Homo sapiens, cytokine CX2 precursor mRNA, complete cds.	AF142410.1	GI:11055014	1078 bp	Linear	PRI 31-OCT-2000
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481	tgagctcaaacccgtgtgagctgtctccaaagactgtgtgtgtgtgtgtgtgtgtgtgtgt	human.	AF142410	Homo sapiens, cytokine CX2 precursor mRNA, complete cds.	AF142410.1	GI:11055014	1078 bp	Linear	PRI 31-OCT-2000
541	tgcggtcaacttcgtgagcggctgtctccaaagactgtgtgtgtgtgtgtgtgtgtgtgtgt	human.	AF142410	Homo sapiens, cytokine CX2 precursor mRNA, complete cds.	AF142410.1	GI:11055014	1078 bp	Linear	PRI 31-OCT-2000
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 156899)  
AUTHORS Kremmidiotis,G., Gardner,A.E., Callen,D.F. and Sutherland,G.R.  
TITLE Large Scale Sequencing of the Chromosome 16 region q24.3  
JOURNAL Unpublished



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Db	18619	CGTGCTGCTGCCGGCTTCCCTTACCTATACATCGGGCTCAGGGCCCCGGAGSGTGGCT	18560
QY	960	cttcccaactcctcttgaagtaacccctglttcttaacaatatttaagtgtaagtgat	1019
Db	18559	CTTCCCAACCTCTTGGAAATACCCCTGTCTTAAACAATATTAAAGTGATACCTGTAT	18500
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RESULT 6  
AC022554

LOCUS	AC022554.2	157090 bp	DNA	LINEAR	1992	2000
DEFINITION	Human sapiens clone Pp11-21B21, WORKING DRAFT SEQUENCE, 35 unordered					
ACCESSION	AC022554					
VERSION	AC022554.2	GI:7637249				
KEYWORDS	HTG; HTGS; PHASE1; HTGS; DRAFT					
SOURCE	human					
ORGANISM	Homo sapiens					

REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS
1 (bases 1 to 157090) Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homio sapiens chromosome, clone RP11-21B21 Unpublished
2 (bases 1 to 157090) Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

COMMENT

TITLE  
JOURNAL

Anderson, S., Baldwin, J., Barina, N., Beekery, K., Beed, F.,  
Boguslavsky, I., Boukpgalter, B., Brown, A., Burkett, G., Castle, A.,  
Chapel, V., Colangelo, M., Collins, S., Collamore, A., Cooke, P.,  
Deceallano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J.,  
Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J.,  
Garfyna, S., Grant, G., Hagos, B., Heatford, A., Horton, L.,  
Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,  
Landers, T., Lenocksky, J., Levine, R., Lien, C., Liu, C., Locke, K.,  
Macdonald, P., Marquis, N., McEwan, P., McGuirk, A., McKeenan, K.,  
McPheeters, R., Meldrum, J., Menus, L., Morrow, J., Naylor, T.,  
Norman, C. H., O'Connor, T., O'Donnell, P., Oliver, T. M., Peterson, K.,  
Pierre, N., Pisanl, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,  
Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,  
Stojanovic, N., Subramanian, A., Talamas, J., Testley, S., Theodore, J.,  
Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wymann, D., Ye, W. J.,  
Zimmer, A. and Zody, M.

Direct Submission

Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Apr 22, 2000 this sequence version replaced 91:5910831.

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Consensus quality: 150850 bases at least Q20
Insert size: 170000; agarose-fp
Insert size: 153690; sum-of-ctrls
Quality coverage: 3.1 in Q20 bases; agarose-fp
Quality coverage: 3.5 in Q20 bases; sum-of-ctrls
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 35 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1 1661: contig of 1661 bp in length
1662 1761: gap of 100 bp
1762 3078: contig of 1317 bp in length
3079 3178: gap of 100 bp
3179 4774: contig of 1596 bp in length
4775 4874: gap of 100 bp
4875 7439: contig of 2565 bp in length
7440 7539: gap of 100 bp
7540 8885: contig of 1346 bp in length
8886 8985: gap of 100 bp
8986 11624: contig of 2639 bp in length
11625 11724: gap of 100 bp
11725 14597: contig of 2873 bp in length
14598 14697: gap of 100 bp
14698 16860: contig of 2163 bp in length
16861 16960: gap of 100 bp
16961 19655: contig of 2695 bp in length
19656 19755: gap of 100 bp
19756 21926: contig of 2171 bp in length
21927 22026: gap of 100 bp
22027 23792: contig of 1766 bp in length
23793 23893: gap of 100 bp
23893 27939: contig of 4047 bp in length
27940 28035: gap of 100 bp
28040 30269: contig of 2230 bp in length
30270 30369: gap of 100 bp
30370 33004: contig of 2635 bp in length
33005 33104: gap of 100 bp
33105 36260: contig of 3156 bp in length
36261 36360: gap of 100 bp
36361 39762: contig of 3402 bp in length
39763 39862: gap of 100 bp
39863 43798: contig of 3936 bp in length
43799 43898: gap of 100 bp
43899 48559: contig of 4661 bp in length
48560 48659: gap of 100 bp
48660 52026: contig of 3367 bp in length
52027 52126: gap of 100 bp
52127 55169: contig of 3043 bp in length
55170 55269: gap of 100 bp
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62414 62513: gap of 100 bp
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71332 71431: gap of 100 bp
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75281 75380: gap of 100 bp
75381 80896: contig of 5516 bp in length
80897 80996: gap of 100 bp
80997 87850: contig of 6854 bp in length
87851 87950: gap of 100 bp
87951 93903: contig of 5953 bp in length
93904 94003: gap of 100 bp
94004 101488: contig of 7485 bp in length
101489 101588: gap of 100 bp
101589 109837: contig of 8249 bp in length

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* 109838 109937: gap of 100 bp
* 109938 116942: contig of 7005 bp in length
* 116943 117042: gap of 100 bp
* 117043 124191: contig of 7149 bp in length
* 124192 124291: gap of 100 bp
* 124292 133924: contig of 9633 bp in length
* 133925 134024: gap of 100 bp
* 134025 144057: contig of 10033 bp in length
* 144058 144157: gap of 100 bp
* 144158 157090: contig of 12933 bp in length.

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## FEATURES

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/clone_lib="RPC1-11 Human Male BAC"
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1762. 3078
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Best Local Similarity 97.7%; Pred. No. 5,8e-125;
Matches 671; Conservative 0; Mismatches 15; Indels 1; Gaps 1;

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QY 421 ggccttcgcagagctgtcgtgtgcagagctgtatcatgtacagagagcgccgcagacagc 480
DB 125189 GGCCTTCCCGCGAGCTCCTGTGCAGAGCGTGTATCATATGACACGAGGCGCCGCGAACAACG 125248
QY 481 tgcgtcaacctcgtgcgtgcgtgtcctcagagctgtgtgtgtgcgcgcgcgcgcctgtc 540
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QY 541 ccgcgacgctcgcgggctcccccacacacttgggaccttgccttcacacacagatcatcca 600
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QY 661 cccctaaagctgacacagctgtgtcctccacagagcgccctattatgtattatgt 720
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DB 125669 CCTGTCTGCTGCTCCCGCTTCCCTTACCTATCTACGTGCTCAGGCCCCGCGAGCTGCT 125728
QY 960 ctccccaacctcctcttgaagtaacccctgttcttcaacaattattaaagtacgtglat 1019
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DB 125789 TATTAACCTGATGAACACATCCCGAGA 125815

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## RESULT 7

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AL591003 221647 bp DNA linear ROD 29-NOV-2001
LOCUS Mouse DNA sequence from clone RP23-354124 on chromosome 13,
DEFINITION complete sequence.
ACCESSION AL591003
VERSION AL591003.16 GI:16605732
KEYWORDS HMG.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 221647)
AUTHORS Kay, M.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2001) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk

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Db 17490 RACSRTGTGTYGTSKMKKKKYSKSRGKMKKTKCYMKMYKRYKTSKCMWYMKSW 17431  
Qy 365 atctaaccttgagataccgtgtgagacaggaatgagaccgtatccacagaagctggcc 424  
Db 17430 GKKRKRCKMKKCTGTRGMSKSSKSGYSKMGMRSSYSTSCWKSCKWYSMMKCKTWS 17371  
Qy 425 ttgcgcagatgctgtgacagagctgtatcgaatgacagagcgagcagagacgtgcg 484  
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Qy 485 ctcaactccgtgctgctgctcagagctgtgtgtgtgctgctgagcgcgcgtctccgcg 544  
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Qy 545 gacgctcgaggtcccccacagcttgagccttgctccacacagatccacagtc 604  
Db 17250 YKSNRRNRNRKTKGTCTNYRRSRAMNMGNAAGCTTCCCANTRNGGGGAAAAAGGC 17191  
Qy 605 cccgtgctgctgacgtgctgctgctgctgctgctgctgctgctgctgctgctgctg 664  
Db 17190 GSASRASCKYKGRMSKSKYRSGTRRCKM-----SKCRGSRGKSMGM 17148  
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Qy 725 tatatgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 784  
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Qy 785 ccccaactgttctccatccatccagctgaatgagtgaggaagacacacacacacac 844  
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Qy 965 caactccttggaagtc 982  
Db 16848 CCACAGGGGGGTAAAGTTC 16831

RESULT 9  
AF429315 125020 bp DNA linear PRI 18-JAN-2002  
LOCUS Homo sapiens junctophilin 3 (JPH3) gene, partial cds.  
DEFINITION AF429315  
ACCESSION AF429315  
VERSION AF429315.1 GI:17646244  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 125020)  
AUTHORS Holmes,S.E., O'Hearn,E., Rosenblatt,A., Callahan,C., Hwang,H.S.,  
Ingersoll,Ashworth,R.G., Fleisher,A., Stevanin,G., Brice,A.,  
Potter,N.T., Ross,C.A. and Margolis,R.L.  
A repeat expansion in the gene encoding junctophilin-3 is  
associated with Huntington disease-like 2  
JOURNAL Nat. Genet. 29 (4), 377-378 (2001)  
MEDLINE 21583737  
PUBMED 11694876  
REFERENCE 2 (bases 1 to 125020)

AUTHORS Holmes,S.E., Ingersoll-Ashworth,R.G., Ross,C.A. and Margolis,R.L.  
TITLE Direct Submission  
JOURNAL Submitted (05-OCT-2001) Psychiatry, Johns Hopkins Medical  
Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA  
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1. 125020  
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BASE COUNT 29056 a 32731 c 30696 g 28283 t 4254 others  
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Best Local Similarity 11.7%; Pred. NO. 0.0085;  
Matches 88; Conservative 315; Mismatches 344; Indels 5; Gaps 1;

Qy 27 cagctgcccgtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 86  
Db 17136 SRSAMCSCYAKKSMCYCYGMSMKGYAYACSRGMSMSKYMGRSTSTGCGCCT 17195  
Qy 87 tgcacacatgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 146  
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Qy 327 cggagaggtgtgtgagagagacacacacacacacacacacacacacacacacacacac 386  
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Qy 447 gctgatatgatacagagagggcgccgagagacgctgctgctgctgctgctgctgctgctg 506  
Db 17551 CCTSRGMSKMRCCCMRGAASSMRAGSMRRKAGKSGWGRKMMWTGGMMSKTYTCT 17610  
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Best Local Similarity 4.5% Pred. No. 0.037,
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Db 1066 TTTTYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1125

QY 663 cctagaccgagacgtgctgctcccaagaggcaccacctattatggtattatgtta 722
Db 1126 TTTTYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1185

QY 723 ttataatgctccccaacacacaccttgggctgggcacatcccgctcgtggaggaca 782
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QY 783 gcccccacattctcctcaatctcacgcctcagtagtctggggtagaaggagctaacac 842
Db 1246 TTTTYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1305

QY 843 ctcttcacgccttaagctcagaaaggctcacagcgtcgtcgtacacctgtctccc 902
Db 1306 TTTTYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1365

QY 903 tgcctgcctccggcttccttaccctacatcacatggcctcagcccgagcgtgctctt 962
Db 1366 TTTTYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1425

QY 963 cccaacctcctggaagacacctgttcttcaacaatt 1001
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ACCESSION	AF458059
VERSION	AF458059.1 GI:18034675

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
Fort,M.M., Cheung,J., Yen,D., Li,J., Zurawski,S.M., Lo,S., Menon,S., Clifford,T., Hunter,B., Lesley,R., Kuchamel,T., Hurst,S.D., Zurawski,G., Leach,M.W., Gorman,D.M. and Rennick,D.M.	
IL-25 induces IL-4, IL-5, and IL-13 and Th2-Associated Pathologies	
In Vivo	
Immunology 15 (6), 985-995 (2001)	
JOURNAL MEDLINE	21629216

PUBMED 11754819  
 REFERENCE 2 (bases 1 to 486)  
 AUTHORS Hurst,S.D., Muchamuel,T., Gorman,D.M., Gilbert,J.M., Clifford,T., Kwan,S., Menon,S., Seymour,B., Jackson,C., Kung,T., Brieand,J., Zurawski,S.M., Chapman,R., Zurawski,G. and Coffman,R.L.  
 TITLE New IL-17 family members promote Th1 or Th2 responses in the lung: In vivo function of the novel cytokine IL-25  
 JOURNAL Unpublished  
 REFERENCE 3 (bases 1 to 486)  
 AUTHORS Gilbert,J.M. and Gorman,D.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (12-DEC-2001) Genomics, DNAX Research Inc., 901 California Ave., Palo Alto, CA 94304, USA

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BASE COUNT 94 a 162 c 141 g 89 t

ORIGIN

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 Db 187 GATGAGACCCCTCAACAGACAGAGGCGCATCTCCCTCGAGATAGATTGGACAGAGACTTG 246  
 QY 401 gaccgtatccacagaagctgacctgcccagagtgccctgtgcagagagctgatatgac 460  
 |||||  
 Db 247 AACCGGCTCCCGCAGACCTGTACACAGCCGCTGTGCTGCCGCGACCTGCACGCCCTA 306  
 QY 461 cggagcggccgcgagacagctgctc---caactccgtgcgctgtctccagagagctgctg 517  
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 Db 307 CAGACAGGCTCCACATGAGACCCCGGGGCACTCGGAGCTGCTTACCAACAGCACT 366  
 QY 518 gtgctgcgcgcgcgcctgtctccgcga 546  
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 Db 367 GTCCTTACCGCGCGGCATGCATGCGCA 395

RESULT 13  
 AX299773 504 bp DNA linear PAT 26-NOV-2001  
 LOCUS AX299773  
 DEFINITION Sequence 1 from Patent WO0179288.  
 ACCESSION AX299773  
 VERSION AX299773.1 GI:17129294  
 KEYWORDS  
 SOURCE unidentified.  
 ORGANISM unidentified.  
 REFERENCE 1 (sites)  
 AUTHORS Hurst,S.D., Zurawski,S.M. and Rennick,D.M.  
 TITLE Cytokine uses; compositions; methods  
 JOURNAL Patent: WO 0179288-A 1 25-OCT-2001;  
 SCHERING CORPORATION (US)  
 FEATURES  
 source  
 1. 504  
 /organism="unidentified"  
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CDS  
 19. 504

/note="unnamed protein product"  
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 PLEPARPRHPECSRASEDGPLNSRAISPMRYELDRDLNRLPQDLYHARCLCPHCVSL  
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mat-peptide 67. 501  
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BASE COUNT 98 a 165 c 148 g 93 t

ORIGIN

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 Best Local Similarity 56.9%; Pred. No. 0.34;  
 Matches 119; Conservative 0; Mismatches 87; Indels 3; Gaps 1;

QY 341 gaggcagacaccaccagcgtccatccaccctgagagataccgltgagacagatgag 400  
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 Db 205 GATGAGACCCCTCAACAGACAGAGGCGCATCTCCCTCGAGATAGATTGGACAGAGACTTG 264  
 QY 401 gaccgtatccacagaagctgacctgcccagagtgccctgtgcagagagctgatatgac 460  
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 Db 265 AACCGGCTCCCGCAGACCTGTACACAGCCGCTGTGCTGCCGCGACTGCCTACAGCTTA 324  
 QY 461 cggagcggccgcgagacagctgctc---caactccgtgcgctgtctccagagagctgctg 517  
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 Db 325 CAGACAGGCTCCACATGAGACCCCGGGGCACTCGGAGCTGCTTACCAACAGCACT 384  
 QY 518 gtgctgcgcgcgcgcctgtctccgcga 546  
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 Db 385 GTCCTTACCGCGCGGCATGCATGCGCA 413

RESULT 14  
 AX253225 644 bp DNA linear PAT 05-OCT-2001  
 LOCUS AX253225  
 DEFINITION Sequence 22 from Patent WO0168705.  
 ACCESSION AX253225  
 VERSION AX253225.1 GI:15986362  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 REFERENCE 1 (bases 1 to 644)  
 AUTHORS Jing,S., Medlock,E., Yeh,R., Silbiger,S.M., Elliott,G.S. and Nguyen,H.O.  
 TITLE IL-17 receptor like molecules and uses thereof  
 JOURNAL Patent: WO 0168705-A 22 20-SEP-2001;  
 Amgen Inc. (US)  
 FEATURES  
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BASE COUNT 144 a 204 c 173 g 123 t

ORIGIN

Query Match 5.1%; Score 53.8; DB 6; Length 644;  
 Best Local Similarity 56.9%; Pred. No. 0.34;  
 Matches 119; Conservative 0; Mismatches 87; Indels 3; Gaps 1;

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 QY 401 gaccgtatccacagagagcgtgcttcgagcagtgctctgacagagcgtatcagtgatga 460  
 DB 405 AACCGGCTCCCGAGAGACCTGTAACACAGCCGCTTGCTGTGCGGACACTGCGTACACCA 464  
 QY 461 cggacggcgcccgagacagctgctc---caactccgtgagcgtgctccagagcctgctg 517  
 DB 465 CAACACAGGCTCCACATGACAGCCCGGAGCACTCGAGAGTGTCTACACACAGCAAGACT 524  
 QY 518 gtgtctgagcgccgagcgtgctcctcccgaga 546  
 DB 525 GTCTTCTACCGGCGGCGCATGCGCA 553

## RESULT 15

LOCUS AY034088 462 bp mRNA linear ROD 03-DEC-2001  
 DEFINITION Mus musculus interleukin 17E precursor, mRNA, partial cds.  
 ACCESSION AY034088  
 VERSION AY034088.1 GI:17266279

## KEYWORDS

house mouse,  
 Mus musculus

## ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 462)  
 Pan, G., French, D., Mao, W., Maruoka, M., Risse, P., Lee, J.,  
 Foster, J., Aggarwal, S., Nicholes, K., Guillet, S., Schow, P. and  
 Gurney, A. L.  
 Forced Expression of Murine IL-17E Induces Growth Retardation,  
 Jaundice, a Th2-Biased Response, and Multiorgan Inflammation in  
 Mice

## JOURNAL

J. Immunol. 167 (11), 6559-6567 (2001)  
 MEDLINE 21571724  
 PUBMED 11714825

## REFERENCE

2 (bases 1 to 462)  
 Pan, G., Mao, W., Maruoka, M., French, D., Risse, P., Lee, J.,  
 Foster, J., Aggarwal, S., Nicholes, K., Guillet, S., Schow, P. and  
 Gurney, A. L.  
 Direct Submission  
 Submitted (08-MAY-2001) Molecular Biology, Genentech, 1 DNA Way,  
 South San Francisco, CA 94080, USA

## FEATURES

Location/Qualifiers

## SOURCE

1..462  
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## CDS

BASE COUNT 90 a 157 c 130 g 85 t  
 ORIGIN

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 Best local Similarity 56.6%; Pred. No. 0.38; Indels 3; Gaps 1;  
 Matches 120; Conservative 0; Mismatches 89;

QY 340 gagcgagacacccacagcgtccatctacacccctgagagataacggtgtgacacagtgatga 399  
 DB 162 GGATGAGCCCTCAACAGACGAGGCGCATCTCTCTTGAGACTATGAGTTGACAGGAGACTT 221

QY 400 gaccgtatccacagagagcgtgcttcgagcagtgctctgacagagcgtatcagtgatga 459  
 DB 222 GATGAGGCTCCCGAGAGACTTGTACACAGCTTGATGCTGTGCGGACACTGCGTACGCT 281  
 QY 460 acgagcgagcgccgagacagctgctc---caactccgtgagcgtgctccagagcctgctg 516  
 DB 282 ACAGACAGGCTCCACATGACAGCCCGTGGCAACTCCGTCACCTTACACACACAGCAAG 341  
 QY 517 gtgtctgagcgccgagcgtgctcctcccgagag 548  
 DB 342 GGTCTTCTACCGGCGGCGCATGCGCA 373

Search completed: September 4, 2002, 01:49:32  
 Job time: 6900 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 4, 2002, 00:42:23 : Search time 202.95 seconds  
(without alignments)  
8857.400 Million cell updates/sec

Title: US-09-854-280-4

Perfect score: 1047

Sequence: 1 gccagagtgtagcagcgctc.....tgatgaacacatcccaaaa 1047

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 1736436 seqs, 858457221 residues 3472872

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : N.Geneseq.032802:\*

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24: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1047	100.0	1047	21	AAA96338
2	1047	100.0	1047	21	AA229728
3	1047	100.0	1047	22	AA546148
4	1047	100.0	1047	22	AA509510
5	1028.4	98.2	1107	21	AAA58991
6	1028.4	98.2	1107	21	AAA59149
7	1006.4	96.1	1067	21	AA236836
8	1006.4	96.1	1067	23	AA167878
9	923.4	88.2	1177	22	AA15291

10	640.4	61.2	705	21	AA236834	Partial nucleotide
11	640.4	61.2	705	23	AA167876	Human interleukin
12	591	56.4	591	21	AAA09153	Human interleukin
13	274.8	26.2	521	21	AAA58990	CDNA encoding a hu
14	273.8	26.2	521	21	AAA58989	CDNA encoding a hu
15	273.8	26.2	521	21	AAA59147	CDNA encoding a hu
16	273.8	26.2	521	21	AAA59148	CDNA encoding a hu
17	230	22.0	230	21	AA229731	Virtual DNA fragment
18	143.8	13.7	332	21	AA236856	CDNA clone HTGED19
19	56.8	5.4	454	21	AAA58982	CDNA encoding a hu
20	56.8	5.4	454	21	AAA59156	CDNA encoding a ra
21	56.8	5.4	522	21	AA236837	Partial nucleotide
22	56.8	5.4	522	23	AA167888	Human interleukin
23	56.8	5.4	1385	21	AAA58983	CDNA encoding a hu
24	56.8	5.4	1385	21	AAA59155	CDNA encoding a hu
25	56.8	5.4	1642	21	AA236835	Partial nucleotide
26	56.8	5.4	1642	23	AA167877	Human interleukin
27	56.8	5.4	1794	22	AA509512	Human CDNA encodin
28	56.8	5.4	1819	21	AA252195	Human transforming
29	56.8	5.4	2361	21	AA252201	Human transforming
30	53.8	5.1	504	21	AAA58986	CDNA encoding a hu
31	53.8	5.1	504	21	AAA59158	CDNA encoding a hu
32	53.8	5.1	504	24	ABA02393	Human interleukin
33	53.8	5.1	644	24	ABA03213	Human IL-17 recept
34	53.6	5.1	985	21	AAA58988	CDNA encoding a mu
35	53.6	5.1	985	21	AAA59160	CDNA encoding a mu
36	53.6	5.1	985	24	ABA02394	Murine interleukin
37	52.2	5.0	1320	22	AA509511	Human CDNA encodin
38	52.2	5.0	1320	22	AA509512	Human CDNA encodin
39	52.2	5.0	1320	22	AA509513	Human CDNA encodin
40	49.8	4.8	1127	21	AAA02477	Human colon cancer
41	49.4	4.7	620	21	AAA58987	CDNA encoding a mu
42	49.4	4.7	2561	22	AA26500	CDNA encoding a mu
43	47.4	4.5	114955	20	AA53491	Rabbit low density
44	47.2	4.5	1032	19	AAV50486	Human adenosine A1
45	46.8	4.5	1032	19	AAV50486	Streptomyces Clavu

## ALIGNMENTS

RESULT 1	AAA96338	standard; cDNA; 1047 BP.
ID	AAA96338	
AC	AAA96338:	
XX		
DT	08-FEB-2001	(first entry)
XX		
DE	cdna encoding a novel polypeptide designated PRO1122.	
XX		
KW	Secreted protein; transmembrane protein; PRO1484; PRO4334; PRO1122;	
KW	PRO1889; PRO1890; PRO1887; PRO1785; PRO4353; PRO4357; PRO4405; PRO4356;	
KW	PRO4352; PRO4380; PRO4354; PRO5737; PRO4425; PRO5990; PRO6030;	
KW	PRO4424; PRO4422; PRO4430; PRO4499; obesity; diabetes;	
KW	Insulinemia; kidney disorder; Bergers disease; nephropathy;	
KW	Schönlein-Henoch purpura; celiac disease; dermatitis herpetiformis;	
KW	Crohn's disease; ss.	
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OS	Homo sapiens.	
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FT		/*tag= a
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PD	MO200056889-A2.	
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XX	28-SEP-2000.	
XX		
XX	01-MAR-2000; 2000WO-US05601.	

PR 23-MAR-1999; 9905-0125774.  
 PR 23-MAR-1999; 9905-0125778.  
 PR 24-MAR-1999; 9905-0125826.  
 PR 31-MAR-1999; 9905-0127035.  
 PR 05-APR-1999; 9905-0127706.  
 PR 21-APR-1999; 9905-0130359.  
 PR 27-APR-1999; 9905-0131270.  
 PR 27-APR-1999; 9905-0131272.  
 PR 04-MAY-1999; 9905-0131291.  
 PR 04-MAY-1999; 9905-0132371.  
 PR 04-MAY-1999; 9905-0132379.  
 PR 04-MAY-1999; 9905-0132383.  
 PR 25-MAY-1999; 9905-0135750.  
 PR 08-JUN-1999; 9905-0138166.  
 PR 20-JUL-1999; 9905-0144791.  
 PR 03-AUG-1999; 9905-0146370.  
 PR 09-DEC-1999; 9905-0170262.

XX (GETH ) GENENTECH INC.

PI Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;  
 PI Stewart TA, Matanabe CK, Wood WI, Zhang Z;

XX WPI, 2000-628263/60.

XX P-PSDB; AAB18911.

PT Novel secreted and transmembrane polypeptides useful for diagnosing  
 PT tumour in a mammal, for identifying agonists and antagonists of the  
 PT polypeptide and for therapeutic use

PS Claim 2; Fig 5; 222pp; English.

XX The present sequence encodes a secreted or transmembrane polypeptide.  
 CC The specification describes polypeptides designated PRO1484, PRO4334,  
 CC PRO1122, PRO1889, PRO1890, PRO1887, PRO1785, PRO4353, PRO4405,  
 CC PRO4356, PRO4352, PRO4380, PRO4354, PRO4357, PRO4425, PRO5990,  
 CC PRO6030, PRO4424, PRO4422, PRO4430 and PRO4499. PRO1889 polypeptide is  
 CC useful for diagnosing tumour in a mammal. The polypeptides, their  
 CC agonists and antagonists are useful treating a condition associated with  
 CC expression or activity of the polypeptide. Conditions treated include  
 CC obesity, diabetes or hyper- or hypo-insulinemia. The polypeptides are  
 CC capable of inducing proliferation of mammalian kidney mesangial cells  
 CC and are therefore useful for treating kidney disorders associated with  
 CC decreased mesangial cell function such as Berger's disease or other  
 CC nephropathies associated with Schönlein-Henoch purpura, celiac disease,  
 CC dermatitis herpetiformis or Crohn's disease. The nucleic acids may be used  
 CC to generate transgenic animals for use in development and screening of  
 CC therapeutically useful reagents and also for chromosome identification  
 CC and tissue typing.

SQ Sequence 1047 BP; 177 A; 381 C; 280 G; 209 T; 0 other;

Query Match 100.0%; Score 1047; DB 21; Length 1047;  
 Best Local Similarity 100.0%; Pred. No. 8.6e-241;  
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 Db 61 ccccgagctctctgttctgacactgtgacacatgtcctgcccacatgaagcctcc 120  
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 OY 661 cccctaaactggagacgt 720  
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 Db 721 tattatattgcttccccacacatacccttgggggtcgtgtgtgtgtgtgtgtgtgtgtgt 780  
 OY 781 cagccccacatgttctccatcattccagcctcagctcagtggtgtgtgtgtgtgtgtgt 840  
 Db 781 cagccccacatgttctccatcattccagcctcagctcagtggtgtgtgtgtgtgtgtgt 840  
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 Db 841 acccttcacagccttaagactgtgagaagaaggtgtacacagcgtcgtgtgtgtgtgtgt 900  
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 Db 961 ttcccaactccttggagaagtaacccctgttcttaacaataatttaagtgtgtgtgt 1020  
 OY 1021 attaaactgtatgaacatccccaataa 1047  
 Db 1021 attaaactgtatgaacatccccaataa 1047

RESULT 2  
 ID AA229728 standard; cDNA; 1047 BP.  
 XX AA229728;  
 XX 27-MAR-2000 (first entry)  
 DE Human Interleukin 17C, PRO1122 cDNA.  
 XX Interleukin, IL-17C; PRO1122 polypeptide; clone DMA62377-1381-1; UNQ561;  
 XX cytokine IL-17; cytotoxic T-lymphocyte-associated antigen 8; CTLA-8;  
 KW hybridisation probe; antagonist; degenerative cartilaginous disorder;  
 KW agonist; diagnosis; therapy; ss.  
 OS Homo sapiens.

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XX Key Location/Qualifiers
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FT mat_peptide 50..634
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FT /label= Mature_Interleukin_17C_polypeptide
FT /note= "Designated as clone DNA62377-1381-1"
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XX MO9960127-A2.
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XX 25-NOV-1999.
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XX 14-MAY-1999; 99MO-US10733.
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XX 15-MAY-1998; 98US-0085579.
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XX 23-DEC-1998; 98US-0113621.
XX
XX (GETH ) GENENTECH INC.
XX
XX PI Chen J, Filvaroff E, Goddard A, Gurney AL, Li H, Wood WT;
XX
XX DR WPI: 2000-116314/10.
XX
XX DR P-PSDB: AAY44460.
XX
XX PT New polypeptides designated PRO1031 and PRO1122 used to treat a
XX
XX PS degenerative cartilaginous disorder -
XX
XX PS Claim 2: Fig 4; 141pp; English.
XX
XX CC The present sequence is the cDNA clone DNA62377-1381-1, encoding the
XX
XX CC human PRO1122 polypeptide, also referred to as UNQ561, and as
XX
XX CC interleukin-17C (IL-17C). This sequence has identity with the
XX
XX CC cytokine IL-17 and cytotoxic T-lymphocyte-associated antigen 8 (CTLA-8).
XX
XX CC PRO1122 is expressed in pancreas, small intestine, stomach and testis
XX
XX CC also. It shares about 26-28% amino acid identity with IL-17 and IL-17B.
XX
XX CC The entire coding region of IL-17C can be used as hybridisation probe.
XX
XX CC The PRO1122 polypeptide, agonist or antagonist, is used to diagnose and
XX
XX CC treat a degenerative cartilaginous disorder.
XX
XX SQ Sequence 1047 BP; 177 A; 381 C; 280 G; 209 T; 0 other;

Query Match 100.0%; Score 1047; DB 21; Length 1047;
Best Local Similarity 100.0%; Pred. No. 8.6e-241;
Matches 1047; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gccagggtgcaagcgcctccaaagccagcctccccgctgcccgcacacatgacgtcct 60
DB 1 gccagggtgcaagcgcctccaaagccagcctccccgctgcccgcacacatgacgtcct 60
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DB 61 ccccgccctcctgttcttgaactgctgacacatgacctgccccacatgacctcct 120
OY 121 caaggggacccccacagtcacgtatccccacactgactgctgaggaactgcct 180
DB 121 caaggggacccccacagtcacgtatccccacactgactgctgaggaactgcct 180
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DB 181 cggcagagccccccacacactgctgctcgaagtgcacagtggggcaggttgcctgt 240
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DB 241 agcccttggtctcagcctgagcagcagccacaggggagcagcagagccctcagc 300
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DB 301 taagacacagtgcccggtgctgcgcgcgagaggtgttgaagcagacacccacagc 360
OY 361 ctccatctcaccttgagataccgtgttgacacagatgagacgctatccacagaagt 420
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OY 421 ggccttcgcagagtgctcctgtgcagagagctgtatcatgacagcagggccgcagacagc 480
DB 421 ggccttcgcagagtgctcctgtgcagagagctgtatcatgacagcagggccgcagacagc 480
OY 481 tgcgtcacaactcctgtgcggtgtgtccacagacctgtgctgtgtgcgcgcgcgcctgtc 540
DB 481 tgcgtcacaactcctgtgcggtgtgtccacagacctgtgctgtgtgcgcgcgcgcctgtc 540
OY 541 ccgcagagcgtcggggctcccccacacactgaggccttgcctccacacacagatcatcca 600
DB 541 ccgcagagcgtcggggctcccccacacactgaggccttgcctccacacacagatcatcca 600
OY 601 cgtcccgctgcgctgacactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 660
DB 601 cgtcccgctgcgctgacactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 660
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DB 661 cccctagactgacacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 720
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DB 721 tattatataatgtcctcccccacacactacccttgggtgtgtgtgtgtgtgtgtgtgtgt 780
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DB 841 acctcttcacgccttaaaagctgcagaaaagtgctacacagcgtgtgtgtgtgtgtgtgt 900
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DB 901 cctgttcctcctccgggtcctcctaccatacagtgctcagggccgcagcgtgtgtgt 960
OY 961 ttcccaactccttggaagtaacccctgttcttaacaatttaagtgatgtgtgt 1020
DB 961 ttcccaactccttggaagtaacccctgttcttaacaatttaagtgatgtgtgt 1020
OY 1021 attaaactgatgaacacatcccaaaa 1047
DB 1021 attaaactgatgaacacatcccaaaa 1047

RESULT: 3
ID AAS46148 standard; cDNA; 1047 BP.
XX AAS46148;
AC AAS46148;
DT 18-DEC-2001 (first entry)
DE Human DNA encoding PRO polypeptide sequence #224.
XX
XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
XX dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
XX blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
XX adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
XX PCR primer.
XX
XX OS Homo sapiens.
XX
XX PN WO200168848-A2.
XX
XX 20-SEP-2001.
XX
XX 28-FEB-2001; 2001WO-US06520.
XX
XX 01-MAR-2000; 2000WO-US05601.
XX
XX 02-MAR-2000; 2000WO-US05841.

```







DB 1021 attaaactgatgacacatcccaaaa 1047

RESULT 4

AA09510

AA09510 standard; cDNA; 1047 BP.

AC AA09510;

DT 24-OCT-2001 (first entry)

XX

DE Human cDNA encoding Interleukin 17C ligand, IL-17C.

XX

KW Human: Interleukin-17C ligand; IL-17C; agonist; antagonist; ss;

KW PRO1122: DNA 62377-1381-1; systemic lupus erythematosus;

KW rheumatoid arthritis; osteoarthritis; diabetes mellitus;

KW allergic disease; asthma; demyelinating disease;

KW degenerative cartilaginous disorder; transplantation associated disease.

XX

OS Homo sapiens.

XX

EH Key Location/Qualifiers

FT CDS 50..643

FT /\*tag= a

FT /product= "IL-17C"

FT sig\_peptide 50..103

FT /\*tag= b

FT mat\_peptide 104..640

FT /\*tag= c

FT /label= Mature\_IL\_17C

XX

PN WO200146420-AZ.

XX

PD 28-JUN-2001.

XX

PF 20-DEC-2000; 2000WO-US34956.

XX

PR 23-DEC-1999; 99US-0172096.

PR 30-DEC-1999; 99WO-US31274.

PR 11-JAN-2000; 2000US-0175481.

PR 18-FEB-2000; 2000WO-US04341.

PR 02-MAR-2000; 2000WO-US05841.

PR 21-MAR-2000; 2000US-0191007.

PR 21-MAR-2000; 2000WO-US07532.

PR 02-JUN-2000; 2000WO-US15264.

PR 22-JUN-2000; 2000US-0213087.

PR 22-AUG-2000; 2000US-0644848.

PR 24-AUG-2000; 2000WO-US23328.

PR 24-OCT-2000; 2000US-0242837.

PR 10-NOV-2000; 2000WO-US30873.

PR 28-NOV-2000; 2000US-0253646.

PR 01-DEC-2000; 2000WO-US32678.

XX

PA (GENETH ) GENENTECH INC.

XX

PI Chen J, Filvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi CJ;

PI Gurney AL, Li H, Hillan KJ, Tamas D, Van Lookeren M, Vandlen RL,

PI Watanabe CK, Williams PM, Wood WI, Yansura DG;

XX

DR WPI: 2001-451708/48.

DR P-PSDB: AAU04951.

XX

PT Novel PRO polypeptides homologous to interleukin-17, useful for the

PT diagnosis and treatment of immune related disease e.g. rheumatoid

PT arthritis and diabetes -

XX

PS Claim 1; Fig 3; 188pp; English.

XX

CC The sequence (DNA 62377-1381-1) encodes a PRO polypeptide (PRO1122)

CC which is the human interleukin 17C ligand, IL-17C. A composition

CC containing ant/agonists to the PRO polypeptides or individual components

CC are useful for treating a mammal with an immune related disease, e.g.

CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,

CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an

CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic

CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune

CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal

CC disease, a demyelinating disease, an autoimmune or immune-mediated skin

CC disease, contact dermatitis, an allergic disease e.g. food

CC hypersensitivity, asthma, a transplantation associated disease, or a

CC chronic inflammatory demyelinating polynuropathy. Treating a PRO1031 or

CC degenerative cartilaginous disorder comprises administering a PRO1031 or

CC PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous

CC examples of the diseases and disorders are given in the specification.

XX

SO Sequence 1047 BP; 177 A; 381 C; 280 G; 209 T; 0 other;

QY

Query Match 100.0%; Score 1047; DB 22; Length 1047;

Best Local Similarity 100.0%; Pred. No. 8.6e-241;

Matches 1047; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 gccaggtgtgacagcgccgccaagccacccctgcccgcgtgcgcacatgacgtcct 60

1 gccaggtgtgacagcgccgccaagccacccctgcccgcgtgcgcacatgacgtcct 60

QY 61 ccccgccctcgttcttctgacctggtgacacatgctcgtgcccacatgacccctcct 120

61 ccccgccctcgttcttctgacctggtgacacatgctcgtgcccacatgacccctcct 120

DB 61 ccccgccctcgttcttctgacctggtgacacatgctcgtgcccacatgacccctcct 120

QY 121 cagggggcaccaccacagtcacagtcacacacgtctactcgtgtgaggaactccct 180

121 cagggggcaccaccacagtcacagtcacacacgtctactcgtgtgaggaactccct 180

DB 121 cagggggcaccaccacagtcacagtcacacacgtctactcgtgtgaggaactccct 180

QY 181 cggcagggcccccacacactgctgctcgaagtgcgaagtggggcagaagcttgcgt 240

181 cggcagggcccccacacactgctgctcgaagtgcgaagtggggcagaagcttgcgt 240

DB 181 cggcagggcccccacacactgctgctcgaagtgcgaagtggggcagaagcttgcgt 240

QY 241 agccctgtgtcagcgttgagcagcagcagcaggggagagcagcagagccctcagc 300

241 agccctgtgtcagcgttgagcagcagcagcaggggagagcagcagagccctcagc 300

DB 241 agccctgtgtcagcgttgagcagcagcagcaggggagagcagcagagccctcagc 300

QY 301 tacgaccagtcgcccgtgtcgtcgccgagagagtggttgagagcagacaccacagcg 360

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DB 301 tacgaccagtcgcccgtgtcgtcgccgagagagtggttgagagcagacaccacagcg 360

QY 361 ctccatctacacctgagatgacgtgtgtgacagcagatgagacggtatccacagaagct 420

361 ctccatctacacctgagatgacgtgtgtgacagcagatgagacggtatccacagaagct 420

DB 361 ctccatctacacctgagatgacgtgtgtgacagcagatgagacggtatccacagaagct 420

QY 421 ggccttcgcagatgctgtgacagagcgtatcagatgacagcagcgcgcgagacagc 480

421 ggccttcgcagatgctgtgacagagcgtatcagatgacagcagcgcgcgagacagc 480

DB 421 ggccttcgcagatgctgtgacagagcgtatcagatgacagcagcgcgcgagacagc 480

QY 481 tgcgtcctaactcgtggtggtgtctccagagcgtgtgtgtgtgtgcgcgcgcgtgtc 540

481 tgcgtcctaactcgtggtggtgtctccagagcgtgtgtgtgtgtgtgcgcgcgcgtgtc 540

DB 481 tgcgtcctaactcgtggtggtgtctccagagcgtgtgtgtgtgtgtgtgcgcgcgcgtgtc 540

QY 541 ccgacagcgtcgggggtcccccacacctgagggccttgcctccacacagagttatcca 600

541 ccgacagcgtcgggggtcccccacacctgagggccttgcctccacacagagttatcca 600

DB 541 ccgacagcgtcgggggtcccccacacctgagggccttgcctccacacagagttatcca 600

QY 601 cgtcccgctcgtgctgacactcgtgtgtgcgcggttcagtgtgacgcgcgagcggtggg 660

601 cgtcccgctcgtgctgacactcgtgtgtgcgcggttcagtgtgacgcgcgagcggtggg 660

DB 601 cgtcccgctcgtgctgacactcgtgtgtgcgcggttcagtgtgacgcgcgagcggtggg 660

QY 661 cccctagactgacacagtgctgtcccccagagggacccctatattatgtattatgt 720

661 cccctagactgacacagtgctgtcccccagagggacccctatattatgtattatgt 720

DB 661 cccctagactgacacagtgctgtcccccagagggacccctatattatgtattatgt 720

QY 721 tattatagctcccccacacactacccttggtgtgtgtgacattcccggtctgtgagga 780

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DB 721 tattatagctcccccacacactacccttggtgtgtgtgacattcccggtctgtgagga 780

QY 781 cagccccccagcttctcctcatctcagcctcagtagttgggggtagaagagcctcagc 840

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 Db 841 acccttccagcccttaaaagctgcagaaaaggtgcacagcgttcctgtaccctgc 900  
 Qy 901 cctgtctgtctccgcgttcctcctacatcagctgcagcgcgcgcgcgcgcgc 960  
 Db 901 cctgtctgtctccgcgttcctcctacatcagctgcagcgcgcgcgcgcgcgc 960  
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 Db 1021 attaacgtatgcatacattccccaaaa 1047

## RESULT 5

AAAS8991  
 ID AAAS8991 standard; cDNA; 1107 BP.

AC AAAS8991;

DT 07-NOV-2000 (first entry)

DE cDNA encoding a human Interleukin (IL) 171 polypeptide.

KM Interleukin; IL-17; CTLA-8; IL-170; IL-172; IL-173; IL-174; IL-176;  
 IL-177; IL-171; cell proliferation; cancer; ss.

OS Homo sapiens.

Key Location/Qualifiers

FT CDS 115..708

FT /product= "Interleukin-171"

FT sig.peptide 115..165

FT mat.peptide 166..705

FT /\*tag= c

PN WO200042188-A2.

PD 20-JUL-2000.

PF 10-JAN-2000; 2000WO-US00006.

PR 11-JAN-1999; 99US-0228822.

PA (SCHE ) SCHERING CORP.

PI Gorman DM, Bazan JF, Kastelein RA;

DR WPI; 2000-466130/40.

DR P-PSDB; AAB07602.

PT New isolated polynucleotide encoding a mammalian Interleukin-17 like

protein used to identify genes for homologous proteins

PS Disclosure; Page 20-21; 111pp; English.

XX The present sequence encodes an Interleukin-171 (IL-171) polypeptide.

XX The polypeptide is an IL-17-like (CTLA-8 related) protein. It is a

XX member of a new group of Interleukins, IL-170 polypeptides. The members

XX comprise IL-172, IL-173, IL-174, IL-176, IL-177, and IL-171.

XX or degenerative conditions. Antibodies can be used in diagnostic

XX methods to detect over production of IL-170 protein in cells or body

XX fluids.

XX Sequence 1107 BP; 183 A; 336 C; 306 G; 222 T; 0 other;

Query Match 98.2%; Score 1028.4; DB 21; Length 1107;  
 Best Local Similarity 99.8%; Pred. No. 2.4e-236;  
 Matches 1040; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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 Qy 61 ccccgacctctgtttctgacctggtgcacacatgcttgccacatgaagccctcct 120  
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 Db 366 taagaccagtgcccggtgtctgcgcggagaggtgtgttgagagcagacacccacagcg 425  
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 Db 426 ctccatcaccttgagatgacctgtgtgacacagatgagacgcgttcacacaaagct 485  
 Qy 421 ggccttcgcagagtgctctgtcagagagctgtatcgaatgcacagagggccgcagacagc 480  
 Db 486 ggccttcgcagagtgctctgtcagagagctgtatcgaatgcacagagggccgcagacagc 545  
 Qy 481 tgcgtcaactcgtggggctgtctcagagcctgtgtgtgtgcgcgcgcgcctgtctc 540  
 Db 546 tgcgtcaactcgtggggctgtctcagagcctgtgtgtgtgcgcgcgcgcctgtctc 605  
 Qy 541 ccgcagaggtctcggggtctcccaacaccttggggccttgccttcacacagagttcatca 600  
 Db 606 ccgcagaggtctcggggtctcccaacacaccttggggccttgccttcacacagagttcatca 665  
 Qy 601 gctcccgctggtcagctgtgctgtcgcgcgttcagatgtgcagccgagagcggtggg 660  
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 Db 726 cccctagactgacacgctgtctcccaagagggacccctattatgtatgtattatgt 785  
 Qy 721 tattatatgctcccccacacataccttgggggtctgggacatcccggtgtctggagga 780  
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 Qy 781 cagcccccaactgtttctcctatctcagcctcagtggtgggtgagaagagctcagc 840  
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 Qy 841 acccttccagcccttaaaagctgcagaaaaggtgcacagcgttcctgtaccctgc 900  
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 Db 966 cctgtctgtctccgcgttcctcctacatcagctgcagcgcgcgcgcgcgcgcgc 1025  
 Qy 960 ctcccaacctctgttggaatgacctgtttcttaacaattatttaagtgcagtgatt 1019  
 Db 1026 ctcccaacctctgttggaatgacctgtttcttaacaattatttaagtgcagtgatt 1085

QY 1020 tattaactgatacaacatcc 1041  
 ||||||||||||||||||  
 DB 1086 tattaactgatacaacatcc 1107

## RESULT 6

AAA59149  
 ID AAA59149 standard; CDNA; 1107 BP.

AC AAA59149;

DT 07-NOV-2000 (first entry)

DE CDNA encoding a human Interleukin-171 polypeptide.

XX Interleukin; IL-171; cytokine; CTLA-8; IL-17; IL-175; IL-172; IL-173;  
 XX IL-174; IL-176; IL-177; cell proliferation; cancer; ss.

OS Homo sapiens.

FX Key Location/Qualifiers  
 FT CDS 115..708

FT /\*tag= a /product= "Interleukin-171"

FT sig\_peptide 115..165

FT /\*tag= b

FT mat\_peptide 166..705

FT /\*tag= c

PN WO200042187-A1.

PD 20-JUL-2000.

XX 10-JAN-2000; 2000WO-US00005.

PR 11-JAN-1999; 99US-0229402.

PA (SCHE) SCHERING CORP.

PI Gorman DM, Bazan JF, Kastelein RA;

DR WPI; 2000-476060/41.

DR P-PSDB; AAB07684.

PT New DNA sequence encoding a mammalian homolog of CTLA-8, designated  
 PT interleukin-171 (IL-171), useful for recombinant production of IL-171  
 PT physiology or development -

PS Claim 1; Page 10-11; 11pp; English.

XX The present sequence encodes an Interleukin (IL)-171 polypeptide. It  
 CC is a mammalian homologue of the cytokine designated CTLA-8 (also  
 CC referred to as IL-17). The specification also describes homologues  
 CC IL-171, IL-175, IL-172, IL-173, IL-174, IL-176, and IL-177. The DNA  
 CC sequence encoding IL-171 is useful for identifying genes, mRNA and  
 CC cDNA molecules which code for related or homologous proteins. The  
 CC IL-171 protein, antibodies against IL-171, and compounds which have  
 CC binding affinity to IL-171 are useful in treatment of conditions  
 CC associated with abnormal physiology or development, including abnormal  
 CC proliferation, e.g. cancerous conditions, or degenerative conditions.  
 CC The IL-171 protein can be used in kits and assay methods for identifying  
 CC compounds that selectively bind to IL-171.

CC Sequence 1107 BP; 183 A; 396 C; 306 G; 222 T; 0 other;

## Query Match

Best Local Similarity 98.2%; Score 1028.4; DB 21; Length 1107;  
 Matches 1040; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 gccaggtgtcagcgctccaagcccgctgcgcgcgcacatgagctcct 60

DB 66 gccaggtgtcagcgctccaagcccgctgcgcgcgcacatgagctcct 125

QY 61 ccccgctcctgtttctgaactgtgtcagacacatgtcgtgccacatgacccctcct 120

DB 126 ccccgctcctgtttctgaactgtgtcagacacatgtcgtgccacatgacccctcct 185

QY 121 caggggagcccccaagcaggtacccccacactgtactgtgctgaggaactgcccct 180

DB 186 caggggagcccccaagcaggtacccccacactgtactgtgctgaggaactgcccct 245

QY 181 cggcagagcccccaacactgtgtcgtgaggtgcacagtgaggcaggtcttgctgt 240

DB 246 cggcagagcccccaacactgtgtcgtgaggtgcacagtgaggcaggtcttgctgt 305

QY 241 agcctgtgttccagcgtgagagcagcaagcaggggagagcagagagccctcagc 300

DB 306 agcctgtgttccagcgtgagagcagcaagcaggggagagcagagagccctcagc 365

QY 301 tacgacccagtgcccggtgtcgcgcgcgcagagaggtgttggagggcagacccacagcg 360

DB 366 tacgacccagtgcccggtgtcgcgcgcgcagagaggtgttggagggcagacccacagcg 425

QY 361 ctccatctcacccttgagagataccgtgtgtgacacagagatgagacccctacacagaagct 420

DB 426 ctccatctcacccttgagagataccgtgtgtgacacagagatgagacccctacacagaagct 485

QY 421 ggccttcgcagagtgctgtgtcagagagctgtatcgatgcagagcggcgcgcagacagc 480

DB 486 ggccttcgcagagtgctgtgtcagagagctgtatcgatgcagagcggcgcgcagacagc 545

QY 481 tgcgtcaactccgtgaggtgtgtctcagagcctgtcgtggtgcgcgcgcgcgcgcgcgc 540

DB 546 tgcgtcaactccgtgaggtgtgtctcagagcctgtcgtggtgcgcgcgcgcgcgcgcgc 605

QY 541 ccgcagagcgtcggggtcctccacacactgtgggccttgcctccacacagagttcacca 600

DB 606 ccgcagagcgtcggggtcctccacacactgtgggccttgcctccacacagagttcacca 665

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QY 661 cccctagactgagcagtggtgtcctccagagagagccctcttatgtgtattatgt 720

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QY 781 cagcccccaactgtctctcctcaatctccagcctcagtagtggggtagaagagctcagc 840

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QY 960 ctcccaactcctcttggaagtacccctgtttcttaacaattatttaagtgtgtagt 1019

DB 1026 ctcccaactcctcttggaagtacccctgtttcttaacaattatttaagtgtgtagt 1085

QY 1020 tattaactgatacaacatcc 1041

DB 1086 tattaactgatacaacatcc 1107

RESULT 7



Db 1021 acaaaaaaaaaa 1032

RESULT 8

ID AA167878 standard. DNA; 1067 BP.

XX AA167878;

XX 13-MAR-2002 (first entry)

DE Human Interleukin (IL)-21 nucleotide sequence.

XX Interleukin; IL-21; IL-22; immunosuppressive; cytostatic; thrombolytic;

KW antinflammatory; antibacterial; gene therapy; human; ds.

XX Homo sapiens.

OS

XX Key Location/Qualifiers

FT CDS 34..627

FT /tag= a

FT /product= "IL-21"

FT sig\_peptide 34..87

FT /tag= c

FT mat\_peptide 88..624

FT /tag= d

XX

PN US2001023070-A1.

XX

PD 20-SEP-2001.

XX

PF 08-DEC-2000; 2000US-0731816.

XX

PR 29-MAY-1998; 98US-087340P.

PR 30-APR-1999; 99US-131365P.

PR 09-DEC-1999; 99US-169837P.

PR 27-MAY-1999; 99US-0320713.

PR 27-MAY-1999; 99WO-US11644.

XX

PA (EBNE/) EBNER R.

PA (RUBE/) RUBEN S M.

PI Ebner R, Ruben SM;

XX

DR WPI: 2001-638470/73.

XX

XX P-PSDB: AAC66121.

XX

PT New interleukin-21 and interleukin-22 polynucleotides and polypeptides,

PT useful for treating, preventing or diagnosing e.g. disorders of

PT hematopoietic cells, autoimmune disorders, or hyperproliferative

PT diseases

XX

PS Claim 2; Fig 6A-B; 87pp; English.

XX

CC The invention relates to novel human proteins designated interleukin

CC (IL)-21 and IL-22. The IL-21 and IL-22 polynucleotides can be used in

CC linkage analysis as a marker for those specific chromosomes, in chromosome

CC mapping, to control gene expression through triple helix formation or

CC antisense DNA or RNA, in gene therapy, in identifying individuals from

CC minute biological samples, as an alternative to restriction fragment

CC length polymorphism (RFLP) analysis, as polymorphic markers for forensic

CC purposes, as molecular weight markers, or as diagnostic probes. IL-21 and

CC IL-22 polypeptides can be used to treat, prevent or diagnose diseases of

CC the immune system by activating or inhibiting the proliferation,

CC differentiation or mobilization of immune cells, disorders of

CC hematopoietic cells (e.g. ataxia, human immunodeficiency virus (HIV)

CC infection, anemia, thrombocytopenia), autoimmune disorders (e.g. Grave's

CC disease, systemic lupus erythematosus, ophthalmia), graft versus host

CC disease, inflammation, hyperproliferative disorders, or infectious

CC diseases. The polypeptides are useful for generating antibodies, which

CC can be used to treat, inhibit or prevent diseases or conditions

CC associated with aberrant expression and/or activity of IL-21 or IL-22.

CC The present sequence represents the full-length nucleotide sequence of

CC human IL-21.

XX

SO Sequence 1067 BP; 215 A; 371 C; 273 G; 206 T; 2 other:

Query Match 96.1%; Score 1006.4; DB 23; Length 1067;

Best Local Similarity 98.9%; Pred. No. 4.4e-231;

Matches 1021; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

QY 17 gctcaagccagcctgcccgcctgcccgcacacagagcctcccccgcctctgttt 76

DB 1 gctcaagccagcctgcccgcctgcccgcacacagagcctcccccgcctctgttt 60

QY 77 ctgacgtgctgacacatgctggcccacacatgacccctccctcaagggggacccccc 136

DB 61 ctgacctgctgacacatgctggcccacacatgacccctccctcaagggggacccccc 120

QY 137 agtcaagctacccacacactgctactcgtgtgaggaactgcccctcgccagggccccc 196

DB 121 agtcaagctacccacacactgctactcgtgtgaggaactgcccctcgccagggccccc 180

QY 197 caactgctgctcgaagtgccaaagtgggggcaagcttgctctgtagccctggtccagc 256

DB 181 caactgctgctcgaagtgccaaagtgggggcaagcttgctctgtagccctggtccagc 240

QY 257 ctggagggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 316

DB 241 ctggagggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 300

QY 317 gtctgctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 376

DB 301 gtctgctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 360

QY 377 agataccgtgtgacacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 436

DB 361 agataccgtgtgacacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 420

QY 437 ctgtgacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 496

DB 421 ctgtgacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 480

QY 497 cggctgctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 556

DB 481 cggctgctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 540

QY 557 ctcccacacactgaggccttgctcctccacacagcagcagcagcagcagcagcagcagcagc 616

DB 541 ctcccacacactgaggccttgctcctccacacagcagcagcagcagcagcagcagcagcagc 600

QY 617 acctgctgctgcccgccttcaatgtgacccgagcagcagcagcagcagcagcagcagcagc 676

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QY 677 gctgctcccccagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 736

DB 661 gctgctcccccagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 720

QY 737 ccaacactaccccttgggtctgggcaatcccgctgtctgagagacagcccccactgttc 796

DB 721 ccaacactaccccttgggtctgggcaatcccgctgtctgagagacagcccccactgttc 780

QY 797 tcttatctccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 856

DB 781 tcttatctccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 840

QY 857 aaagctgcagaaaagtgacacagcagcagcagcagcagcagcagcagcagcagcagcagc 916

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QY 917 ctcccttaacctatcaactgctcagcagcagcagcagcagcagcagcagcagcagcagcagc 975

DB 901 ctcccttaacctatcaactgctcagcagcagcagcagcagcagcagcagcagcagcagcagc 960

Query Match	88.2%	Score 923.4	DB 22	Length 1177
Best Local Similarity	99.8%	Pred. No. 3,1e-211		
Matches 935	Conservative 0	Mismatches 1	Indels 1	Gaps 1
CC and chronic inflammation such as rheumatic diseases, graft versus host disease and multiple sclerosis. IL-17 like antagonists are useful for treating and preventing inflammatory disease, autoimmune disease, allergies, asthma and organ or graft rejection in a patient and also for inhibiting T cell proliferation and/or activation, in vivo B cell proliferation or immunoglobulin secretion, and for blocking the effects of IL-17 in inducing bone destruction. IL-17 like molecule is useful in gene therapy and for mapping the location of the IL-17 like gene and related genes on chromosomes, as hybridisation probes in diagnostic assays. Non human animals in which the promoter for one or more of IL-17 like protein is either activated or inactivated are useful for drug candidate screening. The present sequence is a cDNA encoding human IL-17 like protein.				
SO	Sequence 1177 BP; 206 A; 421 C; 334 G; 216 T; 0 other;			
QY	53	acgcctccccccgagctctgtttcttgacgcgcgcgacacatgctgcccaccatgac	112	
Db	236	agcgcctccccccgagctctgtttcttgacgcgcgcgacacatgctgcccaccatgac	295	
QY	113	ccctccctcaaggaggcaccaccacagtlacagtlacccacactgctactcgctgagaa	172	
Db	296	ccctccctcaaggaggcaccaccacagtlacagtlacccacactgctactcgctgagaa	355	
QY	173	ctgcgcccttcggcaggcccccccaacctgctgtgtcgaagtlgcacaaatgggggaagct	232	
Db	356	ctgcgcccttcggcaggcccccccaacctgctgtgtcgaagtlgcacaaatgggggaagct	415	
QY	233	ttgctgttagcgccttggtgttcacagccttggaaggcagaagccacagggggagcagagag	292	
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QY	293	ccctcagctacagaccagatgcgcggtgtctgcgcgcgcgagggagtggttgaggcagacac	352	
Db	476	ccctcagctacagaccagatgcgcggtgtctgcgcgcgcgagggagtggttgaggcagacac	535	
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Db	536	caccagcgtccatctatccaccctctgagagataccgtgtgacacagatgagagaccgtatcca	595	
QY	413	cagaagcttgacctctgcgcgaagtgacctgtgacagagctgtatcgaatgacagagacggccgc	472	
Db	596	cagaagcttgacctctgcgcgaagtgacctgtgacagagctgtatcgaatgacagagacggccgc	655	
QY	473	gagacagctgctgcctcaactcctgtgcggtgtgtctcagaagccctgcgcgtgtctgcgcgcgg	532	
Db	656	gagacagctgctgcctcaactcctgtgcggtgtgtctcagaagccctgcgcgtgtctgcgcgcgg	715	
QY	533	ccctgcctcccgagcagcgtgcggggtcccccacactctgggggctttgctctccacacag	592	
Db	716	ccctgcctcccgagcagcgtgcggggtcccccacactctgggggctttgctctccacacag	775	
QY	593	ttcatccaagctcccgctgcgtgcacactgcgtgtctgcgcgcgttcagtgtgacgcgcgagg	652	
Db	776	ttcatccaagctcccgctgcgtgcacactgcgtgtctgcgcgcgttcagtgtgacgcgcgagg	835	
QY	653	ccggtggggccctctagacttgagacagctgtgctccccacagaggcaccccctattttgtta	712	
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QY	713	tttatgttattatatalgactccccccaacacataccttggggtcttggtgacattcccggt	772	
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 3, 2002, 23:55:32 ; Search time 48.15 Seconds

(Without alignments)  
5341.190 Million cell updates/sec

Title: US-09-854-280-4

Perfect score: 1047

Sequence: 1 gccacggtgtcagcgcctc.....tgatgacacatccccaacaa 1047

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58.2	5.6	7218	1 US-08-232-463-14	Sequence 14, Appl
2	45.8	4.4	152331	3 US-09-128-155-16	Sequence 16, Appl
3	44.6	4.3	1578	1 US-08-681-129-1	Sequence 1, Appl
4	42.4	4.0	291	4 US-08-931-858E-201	Sequence 201, App
5	42.4	4.0	291	4 US-08-931-858E-202	Sequence 202, App
6	42.4	4.0	471	4 US-08-931-858E-205	Sequence 205, App
7	42.4	4.0	471	4 US-08-931-858E-206	Sequence 206, App
8	41.2	3.9	2588	2 US-08-796-414B-6	Sequence 6, Appl
9	40.8	3.9	291	4 US-08-931-858E-199	Sequence 199, App
10	40.8	3.9	291	4 US-08-931-858E-200	Sequence 200, App
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12	40.8	3.9	471	4 US-08-931-858E-204	Sequence 204, App
13	40.8	3.9	3695	1 US-08-091-569-1	Sequence 1, Appl
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15	40.8	3.9	3695	2 US-08-822-238-1	Sequence 1, Appl
16	40.8	3.8	319	4 US-09-165-264-8	Sequence 8, Appl
17	39.6	3.8	320	4 US-09-165-264-14	Sequence 14, Appl
18	39.4	3.8	5115	3 US-08-348-518C-3	Sequence 3, Appl
19	39.4	3.8	5115	3 US-08-476-509B-3	Sequence 3, Appl
20	38.8	3.7	267	4 US-08-931-858E-222	Sequence 222, App
21	38.6	3.7	5822	3 US-08-899-595-4	Sequence 4, Appl
22	38.6	3.7	5822	3 US-08-899-595-5	Sequence 5, Appl
23	38.6	3.7	71989	4 US-09-443-501A-2	Sequence 2, Appl
24	38.2	3.6	1659	3 US-09-083-351-3	Sequence 3, Appl
25	38.2	3.6	1659	4 US-09-083-352-3	Sequence 3, Appl
26	38.2	3.6	3946	3 US-09-083-351-1	Sequence 1, Appl
27	38.2	3.6	3946	4 US-09-083-352-1	Sequence 1, Appl

28	38	3.6	1271	4 US-09-231-227-1	Sequence 1, Appl
29	37.8	3.6	318	4 US-09-165-264-12	Sequence 12, Appl
30	37.8	3.6	320	4 US-09-165-264-13	Sequence 13, Appl
31	37.8	3.6	822	4 US-09-228-986-38	Sequence 38, Appl
32	37.6	3.6	320	4 US-09-165-264-7	Sequence 7, Appl
33	37.4	3.6	320	4 US-09-165-264-11	Sequence 11, Appl
34	37.4	3.6	405	2 US-08-903-800A-3	Sequence 3, Appl
35	37	3.5	12001	1 US-08-458-568A-11	Sequence 11, Appl
36	37	3.5	44377	2 US-08-804-227C-7	Sequence 7, Appl
37	37	3.5	44377	2 US-08-804-198-1	Sequence 1, Appl
38	37	3.5	68750	3 US-09-335-409-1	Sequence 1, Appl
39	37	3.5	68750	4 US-09-568-102-1	Sequence 1, Appl
40	37	3.5	68750	4 US-09-567-969-1	Sequence 1, Appl
41	37	3.5	68750	4 US-09-568-480-1	Sequence 1, Appl
42	37	3.5	68750	4 US-09-568-486-1	Sequence 1, Appl
43	37	3.5	68750	4 US-09-568-472-1	Sequence 1, Appl
44	36.8	3.5	2580	3 US-09-050-863-2	Sequence 2, Appl
45	36.8	3.5	2580	4 US-09-335-081-2	Sequence 2, Appl

#### ALIGNMENTS

RESULT 1  
US-08-232-463-14  
Sequence 14, Application US/08232463  
Patent No. 5670367  
GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHERLINGER, F.  
APPLICANT: FALKNER, F. G.  
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)636-9300  
TELEFAX: (703)683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: pTZgpt-F15  
US-08-232-463-14

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	Best Local Similarity	50.78	Pred. No.	0.067;	
	Matches 110;	Conservative	0;	Mismatches 107;	Indels 0;
QY	18	ctcaagcccagcgtccgcgcttgcgcgcacatgagctcttcgccgcctctgtttc	77		
Dh	22086	cccgagccccccgccccccccccggcagcgaggccccccccccgccccgcgcgcgcgc	22145		
QY	78	tgaactgctgctcacatcgtctgcccacatgacctctcataggaggaccaccaca	137		
Dh	22146	gcacgcccgagcccccccccgcg cccgcgcccgcccccccccccgccccccccccgcgc	22205		

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	Best Local	Similarity	46.7%	Pred. No.	0.029	
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QY	242	gacctgtgtctcagcccttgtaggcacgaaccacagggggagcacgagagccctagt	301			
Db	457	GGCTTGSTGACGCCGTGAACAGAGCCCTTCGCCCTGGTGCAGGGGTACTCCTCCGAG	516			
QY	302	aagaaaccagatgcccggtgctgcgcgcggagaggttgtltttagagcaaacaccacacagcgc	361			
Db	517	CTGCCCAAGCTCGCATCAGAGTGCTGACGAGGGGGCTTTTAGCGCAATCCCCGGCGTCCC	576			
QY	362	tcatattcaacctgtgatataccggtgtlgtgacaacgagatagaaccgcgtatccaagaagctgt	421			
Db	577	CC---CCCGCTTAGGGGGAGAACGGGGCCACAGCGCCCTGTGTGTGAAGGGGGGGCGGG	633			



```

CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MO
COUNTRY: USA
ZIP: 63105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,858E
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 971486
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 206:
SEQUENCE CHARACTERISTICS:
LENGTH: 471 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-931-858E-206

Query Match          4.0%; Score 42.4; DB 4; Length 471;
Best Local Similarity 55.4%; Pred. No. 0.068; Mismatches 66; Indels 0; Gaps 0;
Matches      82; Conservative    0; Mismatches     66; Indels     0; Gaps     0;

QY   410 ccacgaagctgctgcgttcgcagatgacctgtgcagaaggctgatcatgacagcagcgcc 469
       ||||| | | | | | ||||| | | | | | ||||| | | | | | |||||
DB   8 CCACGCCCGCACGAGCCGCCGCAGACTGGGGCACCCTGCCACCGGTGGCGTCAATCG 67
QY   470 cgcgagacagctgcgctcaactcgttgcggctgcctccagagctcttgtagtgcgccg 529
       || | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB   68 AGGAGGCCACACTCGTGTAAGCATGTGGGCCGCGACAGGGCCCCCGCGGAGCTCGGCC 127
QY   530 cgagcctgctccgcgcgacgagctcgagcc 557
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DB   128 TGGCCCTGCAGCCGGCGCCAGCGCCAGCG 155

RESULT      8
US-08-796-41A-B-6
Sequence 6, Application US/0879641AB
Patent No. 5876987
GENERAL INFORMATION:
APPLICANT: Wendy C. Champness, Paul Brian
APPLICANT: and Todd B. Anderson
TITLE OF INVENTION: METHOD, DNA AND BACTERIA
FOR HYPERPRODUCTION OF AN ANTIBIOTIC DUE TO DISRUPTION OF AN AbsA GENE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
CITY: Okemos
STATE: Michigan
COUNTRY: USA
ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
COMPUTER: Acer

```



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RESULT      9
US-08-931-858E-199/c
; Sequence 199, Application US/08931858E
; Patent No. 6222022
; GENERAL INFORMATION:
APPLICANT: JOHNSON, EUGENE M
APPLICANT: MILBRANDT, JEFFREY D
APPLICANT: KOTZBAUER, PAUL T
APPLICANT: LAMPE, PATRICIA A
APPLICANT: KLEIN, ROBERT
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MO
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,858E
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 971486
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-931-858E-199

Query Match          3.9%; Score 40.8; DB 4; Length 291;
Best Local Similarity 54.7%; Pred. No. 0.15;
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Db  284 CCACAGCGCCGACGAGCGGCCGACGAGCTGGGGCACCCGCTGCACAGCGGTGGCGTCATCG 225
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QY  470 cgcgagacagctggtcctaactcgttgcggctgtctccagagacctgtgttgttgcgcgc 529
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db  224 AGGAAGGCGCAGCTCGTGTAAGCAATGGGCGGACAGAGGCCCCAACCCTGGGCTCGGCC 165
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QY  530 cgagccctgctcccgagcaagctcgggcg 557
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RESULT      10
US-08-931-858E-200
; Sequence 200, Application US/08931858E
; Patent No. 6222022
; GENERAL INFORMATION:
APPLICANT: JOHNSON, EUGENE M
APPLICANT: MILBRANDT, JEFFREY D
APPLICANT: KOTZBAUER, PAUL T
APPLICANT: LAMPE, PATRICIA A
APPLICANT: KLEIN, ROBERT
```

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1  COMPUTER READABLE FORM:
2  MEDIUM TYPE: Floppy disk
3  COMPUTER: IBM PC compatible
4  OPERATING SYSTEM: PC-DOS/MS-DOS
5  SOFTWARE: PatentIn Release #1.0, Version #1.30
6  CURRENT APPLICATION DATA:
7  APPLICATION NUMBER: US/08/931,858E
8  FILING DATE:
9  CLASSIFICATION: 435
10 ATTORNEY/AGENT INFORMATION:
11 NAME: HOLLAND, DONALD R.
12 REGISTRATION NUMBER: 35,197
13 REFERENCE/DOCKET NUMBER: 971486
14 TELECOMMUNICATION INFORMATION:
15 TELEPHONE: 314-727-5188
16 TELEFAX: 314-727-6092
17 INFORMATION FOR SEQ ID NO: 203:
18 SEQUENCE CHARACTERISTICS:
19 LENGTH: 471 base pairs
20 TYPE: nucleic acid
21 STRANDEDNESS: single
22 TOPOLOGY: linear
23 MOLECULE TYPE: cDNA
24 US-08-931-858E

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	Query Match	Best Local Similarity	Score	DB	Length
	Matches	%			
	81;	Conservative	54.7%;	Pred No.	0.17; Mismatches 67; Indels 0; Gaps 0;
QY	410	ccacagaagctggtccttcgcgcgagtgcctgttcaagaagctatcatgatgaacgagcggc	469		
Db	464	CCACAGGCCGAGGCACCGCCCGAGAAGCTGGGGCACCCTCCAGCGGTGGCGTATTCG	405		
QY	470	cgcgagacagctgcgtctcaactccgtgcggtgcgtgtccaagacctgtgtgtctgcgcgc	529		
Db	404	AGGAAGGCCACGTCGGTGTCAGCAATGGGGCCGCGAGCAGGGCCACACGTTGGGCTGGCCC	345		
QY	530	cggcgctgtgcccgagcagcgtccggggc	557		
Db	344	TGGCCCTGCACGCCGGGCCACGCCCACGGC	317		

RESULT 12  
US-08-931-858E-204  
Sequence 204, Application US/08931858E  
Patent No. 6222022  
GENERAL INFORMATION:  
APPLICANT: JOHNSON, EUGENE M  
APPLICANT: MILLBRAND, JEFFREY D  
APPLICANT: KOTZBAUER, PAUL T  
APPLICANT: LAMPE, PATRICIA A  
APPLICANT: KLEIN, ROBERT  
APPLICANT: DESAVAGE, FRED  
TITLE OF INVENTION: PERSPHIN AND RELATED GROWTH FACTOR  
NUMBER OF SEQUENCES: 239  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
CITY: ST. LOUIS  
STATE: MO  
COUNTRY: USA  
ZIP: 63105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/931,858E  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 971486  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 314-727-5188  
TELEFAX: 314-727-6092  
INFORMATION FOR SEQ ID NO: 204:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 471 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-931-858E-204

Query Match 3.9%; Score 40.8; DB 4; Length 471;  
Best Local Similarity 54.7%; Pred. No. 0.17;  
Matches 81; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

OY 410 cccagagacgtgacctgacgagctgctgacagagctgctgacgagcggc 469  
DB 8 CCACACCCACAGACACCCCGGAGCTGGGGCGCCGCGCCAGCGGCGGTGATCG 67  
OY 470 cgcgagacagctgctgacacacacacacacacacacacacacacac 529  
DB 68 AGAAGAGCCACGTCGTGTAGGAGAGTGGGCGCGGACGACGAGCGCCACCGTGGGCC 127  
OY 530 cgcgacctgctcccgagcagcgtcggagc 557  
DB 128 TGCCCTGCAGCGCGGCGCCAGCGCCAGCG 155

## RESULT 13

US-08-091-569-1  
Sequence 1, Application US/08091569

Patent No. 5494792

GENERAL INFORMATION:

APPLICANT: KAMBOJ, Rajender

APPLICANT: NUTT, Stephen

APPLICANT: SHEKTER, Lee

APPLICANT: WOSNICK, Michael

TITLE OF INVENTION: KAINATE-BINDING HUMAN CNS RECEPTORS OF

TITLE OF INVENTION: THE EAA2 FAMILY

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 1800 Diagonal Road, Suite 500

CITY: Alexandria

STATE: Virginia

COUNTRY: USA

ZIP: 22313-0299

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/091,569

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/750,081

FILING DATE: 27-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 16777/149/ALLE

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)836-9300

TELEFAX: (703)836-4109

TELEX: 899149

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 3695 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 176..229  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 230..3118  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 176..3118  
US-08-091-569-1

Query Match 3.9%; Score 40.8; DB 1; Length 3695;  
Best Local Similarity 51.7%; Pred. No. 0.35;  
Matches 93; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

OY 518 gtgtgtgagc 577  
DB 2879 GCGCAGCGGGGGCGCCGAGCGCTCTGAGAGACCCCGGGCGCCGAGCCGACCC 2938  
OY 578 gcttccacacagagctgacacacacacacacacacacacacacacac 637  
DB 2939 GCGGCCCCACCCCTGCACCCAGTGGCGGTGCGAGAGTCCGGGCGATCCAGCGG 2998  
OY 638 gtgtgacgc 697  
DB 2999 CTGCGGGGCTCGGGGGCGCGCGCGCTCGCGGTGGCGCTCCCGCGAGCGCACCC 3058

## RESULT 14

US-08-203-676-1

Sequence 1, Application US/08203676

Patent No. 5614406

GENERAL INFORMATION:

APPLICANT: KAMBOJ, Rajender

APPLICANT: NUTT, Stephen

APPLICANT: SHEKTER, Lee

APPLICANT: WOSNICK, Michael

TITLE OF INVENTION: KAINATE-BINDING HUMAN CNS RECEPTORS OF

TITLE OF INVENTION: THE EAA2 FAMILY

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 1800 Diagonal Road, Suite 500

CITY: Alexandria

STATE: Virginia

COUNTRY: USA

ZIP: 22313-0299

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/203,676

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/750,081

FILING DATE: 27-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 16777/149/ALLE

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)836-9300

TELEFAX: (703)836-4109

## RESULT. 15

; GENERAL INFORMATION:

STATE: D.C.

ZIP: 20007-5109

COMPUTER READABLE FORM

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA: SOFTWARE: PatentIn Release #1.0,

APPLICATION NUMBER: ITS/08/822-238

FILING DATE: 20-MAR-1991

CLASSIFICATION: 435

PRIOR APPLICATION DATA: . . .

APPLICATION NUMBER: US 08/203,676

FILED DATE: 28-FEB-1994

APPLICATION NUMBER: US 07/750 061

FILING DATE: 27-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A..

10

10

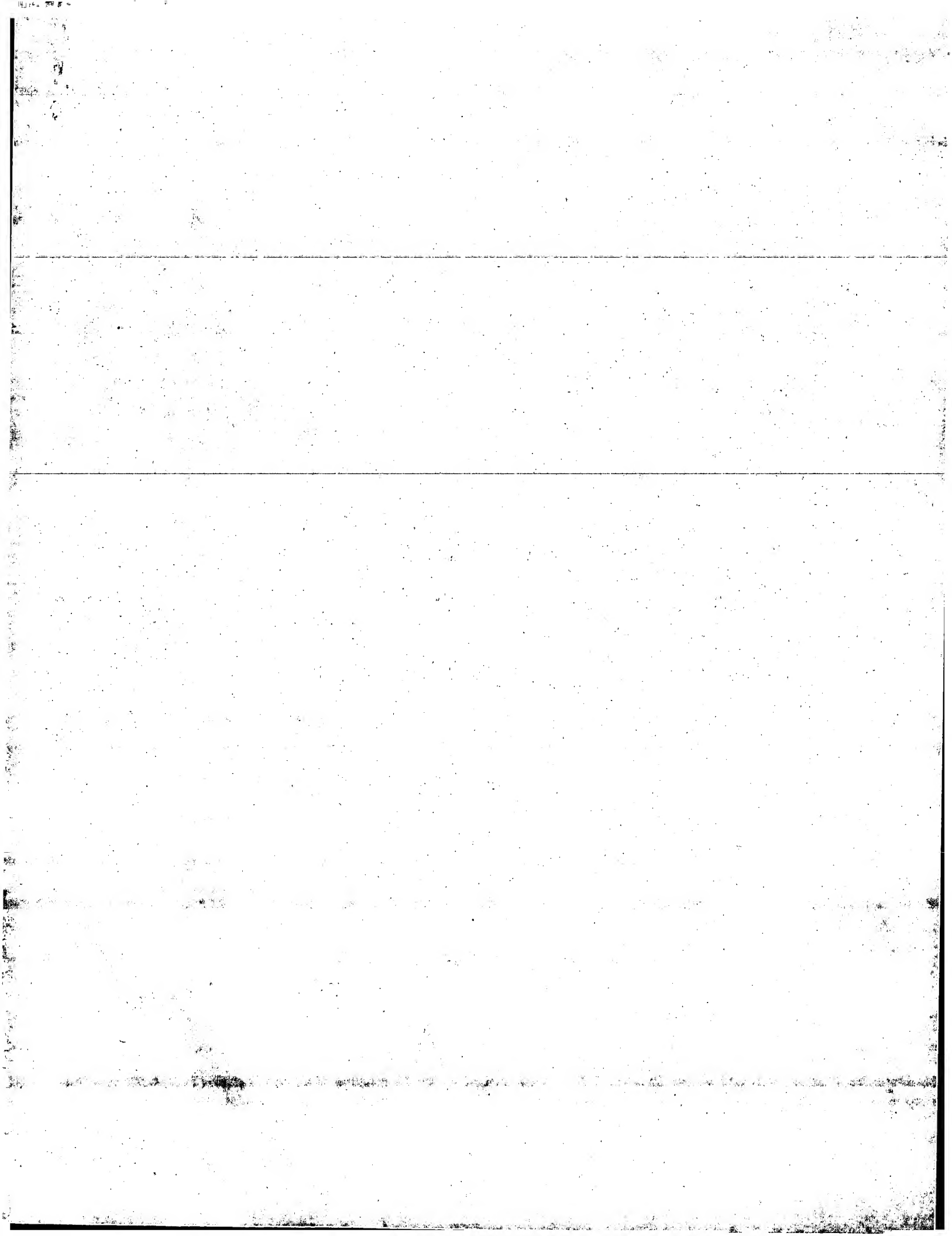
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1 REGISTRATION NUMBER: 29,768
2 REFERENCE/DOCKET NUMBER: 16777/304
3 TELECOMMUNICATION INFORMATION:
4 TELEPHONE: (202)672-5300
5 TELEFAX: (202)672-5399
6 TELEX: 904136
7 INFORMATION FOR SEQ ID NO: 1:
8 SEQUENCE CHARACTERISTICS:
9 LENGTH: 3695 base pairs
10 TYPE: nucleic acid
11 STRANDEDNESS: double
12 TOPOLOGY: linear
13 MOLECULE TYPE: DNA (genomic)
14 FEATURE:
15 NAME/KEY: sig_peptide
16 LOCATION: 176..229
17 FEATURE:
18 NAME/KEY: mat_peptide
19 LOCATION: 230..3115
20 FEATURE:
21 NAME/KEY: CDS
22 LOCATION: 176..3115
23 US-08-822-238-1
24
25 Query Match 3.9%; Score 40.8; DB 2; Length 3695;
26 Best Local Similarity 51.7%; Pred. No. 0.35;
27 Matches 93; Conservative 0; Mismatches 87; Indels 0; Gaps 0.
28
29 QY 518 gtgtgtgacccgcgcgcctgtctccgcgacagcgtcgtgggctcccaacacttgggccttt 577
30 Db 2879 GCGGACGCGGGGCGCCGACGAGGCGCTCTGAGACGACCCGGGGCCCCCAGCGAGCCGACCC 2938
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32 QY 578 gcccttcacacgcagatcattccaaagtccctcccgctggcgtgcacctgctgltgtcccggttca 637
33 Db 2939 GCGGCCCCCAGCCCGCTGCACCCACGCTGGCGCTGTGCGCAGAGTGCTCGGGCATTCAGAGCG 2998
34
35 QY 638 gtgtgacgcgcgcgcgcgtgtggggccctctagacttgacacgctgtgtctcccaaggagcacc 697
36 Db 2999 CTCGCGGCGCTCGGGGGCCCGGCGCGCTCTCCGCGTGGCCTGGGCGTGCCTCCGCGCAAGCCACC 3058

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Search completed: September 4, 2002, 01:47:21  
Job time: 6709. sec





GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 3, 2002, 23:50:42 ; Search time 1611.71 seconds  
(without alignments)  
8767.900 Million cell updates/sec

Title: US-09-854-280-4  
Perfect score: 1047  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :  
EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	377	36.0	669	12 AG139411	AG139411 Pan trogl
C 2	244.8	23.4	264	10 BE551188	BE551188 7b55903.x
C 3	66	6.3	1203	12 CNS01574	AL106054 Drosophill
C 4	58.6	5.6	873	12 AG043471	AG043471 Pan trogl
C 5	58	5.5	1452	12 AG032979	AG032979 Pan trogl
C 6	56.8	5.4	441	9 AI275406	AI275406 q163c10.x
C 7	56.8	5.4	836	10 B1828970	B1828970 603074846
C 8	56.4	5.4	1520	12 AG057334	AG057334 Pan trogl
C 9	55.8	5.3	932	12 CNS00720	AL066742 Drosophill
C 10	55.6	5.3	925	12 CNS0091P	AL053013 Drosophill
C 11	55.2	5.3	524	9 AI430337	AI430337 m168b10.y
C 12	55.2	5.3	718	10 B1561289	B1561289 603256441
C 13	54.8	5.2	1137	10 BG809979	BG809979 mgct002xd
C 14	54.6	5.2	925	12 CNS0091P	AL053013 Drosophill
C 15	54.4	5.2	862	12 AG036151	AG036151 Pan trogl
C 16	52.6	5.0	435	10 BG579143	BG579143 df23f12.y
C 17	52.6	5.0	673	9 AL577596	AL577596 AL577596

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19	52.2	5.0	1025	12 <th>CNS031M</th> <th>AL249701 Tetradon</th>	CNS031M	AL249701 Tetradon
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C 22	51.2	4.9	910	12 <th>AG032931</th> <th>AG032931 Pan trogl</th>	AG032931	AG032931 Pan trogl
C 23	50.8	4.9	832	12 <th>AG132251</th> <th>AG132251 Pan trogl</th>	AG132251	AG132251 Pan trogl
C 24	50.8	4.9	989	12 <th>AG030675</th> <th>AG030675 Pan trogl</th>	AG030675	AG030675 Pan trogl
C 25	50.6	4.8 <td>1081</td> <td>9 <th>AW727480 GA_Ea001</th> <th>AW727480 GA_Ea001</th> </td>	1081	9 <th>AW727480 GA_Ea001</th> <th>AW727480 GA_Ea001</th>	AW727480 GA_Ea001	AW727480 GA_Ea001
C 26	50.4	4.8 <td>1101</td> <td>12 <th>CNS00397</th> <th>AL063912 Drosophill</th> </td>	1101	12 <th>CNS00397</th> <th>AL063912 Drosophill</th>	CNS00397	AL063912 Drosophill
C 27	50.2	4.8 <td>868</td> <td>3 <th>B1644484</th> <th>B1644484 Op2219.Mt</th> </td>	868	3 <th>B1644484</th> <th>B1644484 Op2219.Mt</th>	B1644484	B1644484 Op2219.Mt
C 28	50.2	4.8 <td>957</td> <td>10 <th>BH416095</th> <th>BH416095 Op21179.M</th> </td>	957	10 <th>BH416095</th> <th>BH416095 Op21179.M</th>	BH416095	BH416095 Op21179.M
C 29	50.2	4.8 <td>1077</td> <td>12 <th>CNS0156Q</th> <th>AL105068 Drosophill</th> </td>	1077	12 <th>CNS0156Q</th> <th>AL105068 Drosophill</th>	CNS0156Q	AL105068 Drosophill
C 30	50	4.8 <td>844</td> <td>12 <th>CNS0052P</th> <th>AL056652 Drosophill</th> </td>	844	12 <th>CNS0052P</th> <th>AL056652 Drosophill</th>	CNS0052P	AL056652 Drosophill
C 31	49.4	4.7 <td>420</td> <td>10 <th>W88186</th> <th>W88186 m168b10.r1</th> </td>	420	10 <th>W88186</th> <th>W88186 m168b10.r1</th>	W88186	W88186 m168b10.r1
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C 34	49	4.7 <td>664</td> <td>12 <th>BH140735</th> <th>BH140735 ZM8BD000</th> </td>	664	12 <th>BH140735</th> <th>BH140735 ZM8BD000</th>	BH140735	BH140735 ZM8BD000
C 35	49	4.7 <td>839</td> <td>12 <th>CNS004NB</th> <th>AL054280 Drosophill</th> </td>	839	12 <th>CNS004NB</th> <th>AL054280 Drosophill</th>	CNS004NB	AL054280 Drosophill
C 36	49	4.7 <td>840</td> <td>12 <th>B19033</th> <th>B19033 T28M6-Sp6.T</th> </td>	840	12 <th>B19033</th> <th>B19033 T28M6-Sp6.T</th>	B19033	B19033 T28M6-Sp6.T
C 37	49	4.7 <td>848</td> <td>12 <th>AG060231</th> <th>AG060231 Pan trogl</th> </td>	848	12 <th>AG060231</th> <th>AG060231 Pan trogl</th>	AG060231	AG060231 Pan trogl
C 38	49	4.7 <td>993</td> <td>12 <th>AG090948</th> <th>AG090948 Pan trogl</th> </td>	993	12 <th>AG090948</th> <th>AG090948 Pan trogl</th>	AG090948	AG090948 Pan trogl
C 39	49	4.7 <td>1030</td> <td>12 <th>AG077951</th> <th>AG077951 Pan trogl</th> </td>	1030	12 <th>AG077951</th> <th>AG077951 Pan trogl</th>	AG077951	AG077951 Pan trogl
C 40	48.8	4.7 <td>724</td> <td>12 <th>AG171201</th> <th>AG171201 Pan trogl</th> </td>	724	12 <th>AG171201</th> <th>AG171201 Pan trogl</th>	AG171201	AG171201 Pan trogl
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C 42	48.8	4.7 <td>952</td> <td>12 <th>CNS0766T</th> <th>AL431019 T7 end of</th> </td>	952	12 <th>CNS0766T</th> <th>AL431019 T7 end of</th>	CNS0766T	AL431019 T7 end of
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C 44	48.6	4.6 <td>421</td> <td>12 <th>BH254057</th> <th>BH254057 SALK1059</th> </td>	421	12 <th>BH254057</th> <th>BH254057 SALK1059</th>	BH254057	BH254057 SALK1059
C 45	48.4	4.6 <td>744</td> <td>12 <th>CNS0172K</th> <th>AL108698 Drosophill</th> </td>	744	12 <th>CNS0172K</th> <th>AL108698 Drosophill</th>	CNS0172K	AL108698 Drosophill

## ALIGNMENTS

RESULT 1  
LOCUS AG139411/C  
DEFINITION Pan troglodytes DNA, clone: PTB-153006.F, genomic survey sequence.  
ACCESSION AG139411  
VERSION AG139411.1 GI:16669089  
KEYWORDS GSS; GSS (genome survey sequence).  
SOURCE Pan troglodytes male lymphoblast DNA, clone\_1lb:PTB Chimpanzee Male  
BAC library clone:PTB-153006.F.  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

REFERENCE  
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
Totoki,Y., Watanabe,H. and Sakaki,Y.

TITLE BAC end sequences of library PTB  
JOURNAL Unpublished

REFERENCE  
AUTHORS 2 (bases 1 to 669)  
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
Totoki,Y., Watanabe,H. and Sakaki,Y.

TITLE Direct Submission  
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail:chimbases@sc.riken.go.jp, URL:http://ngp.gsc.riken.go.jp/,  
Tel:81-45-503-9111, Fax:81-45-503-9170)

COMMENT  
Clones are derived from the chimpanzee BAC library PTB This BAC end  
was generated during the R&D process and may have higher chance of  
clone tracking errors.  
PRIMERS  
Sequencing: -21M13  
LIBRARY  
Vector : pKS145  
R.Site 1 : SacI  
R.Site 2 : SacI  
Location/Qualifiers  
1. 669  
/organism="Pan troglodytes"  
/db\_xref="taxon:9598"  
/clone="PTB-153006.F"

FEATURES  
source







[illegible]

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OY	481	t-----gcgtcaactcgtctgagctgtctccagaagacctgtgttctgttcgcgcgcggc	534
Db	1189	NCGCGCGCGCGCGCNMGCCCGCGCGCMGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	1248
OY	535	ctgtctccgcgcagacggtctgaggctccccacaacctggggccttttgctctccaacagagt	594
Db	1249	CGCCG	1308
OY	555	caccacgctcccgcgtcgagctgtcacctcgtgttgttctgcccttcatgtgtgaccgcgaag	651
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RESULT	6		
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ACCESSION	A1275406	sequence.	
VERSION	A1275406.1	GI:3897680	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1. (bases 1 to 441)		
JOURNAL	NCI-CGAP http://www.ncbi.nlm.nih.gov/cgi/gap.		
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgabs-r@mail.nih.gov This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1146 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 428. Location/Qualifiers 1..441 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:1877010" /clone_1lb="Soares_NHMPU_SI" /tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus" /lab_host="DH10B" /note="(Organ: mixed (see below); Vector: pRTT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NBHM, pregnant uterus NBHPU, and fetal heart NBH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of T.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."		
BASE COUNT	63 a 174 c 143 g 61 t		
ORIGIN			
Query Match	5.4%	Score 56.8; DB 9; Length 441;	
Best Local Similarity	51.2%;	Pred. No. 0.14;	
Matches 133:	Conservative 0; Mismatches 127; Indels 0; Gaps 0;		
OY	349	caccaccagcgtccatccatccacctgagatagctgtgtagaacagatagaccgcta	408
Db	152	CACCACCTGTGGCAAGCGTGTCGGCCTCACGAATCTCTCCACGACCCCGGAGTA	211
OY	409	tccacagaagctgtgccttcgcgcagatgcctgtgtcacagaagctgatatcgaatcacagcagc	468









Db 710

QY 245 ctgtgtccagcctgtagcagcaagccacaggggaggcacgagagccctcagctacg 304



[illegible]

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Search completed: September 4, 2002, 01:14:31
Job time: 5029 sec
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Db 60 MSRNIESRSTSPWNTYVTDPRYSEVVOACRNLGGINAO-GKEDISMSVPIQOETL 118  
QY 157 VLRR--PCSRDSSGLPTGAFATFTEFHVPVGTCTVLP 194  
Db 119 VVRRKHQGS-----VSFOLEKVLTVVGTCTVLP 147

## RESULT 2

US-08-833-823-12  
Sequence 12, Application US/08833823  
Patent No. 5969093

GENERAL INFORMATION:  
APPLICANT: Jacobs, Kenneth  
APPLICANT: McCoy, John  
APPLICANT: Kelleher, Kerry  
APPLICANT: Carlin, McKeough  
TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02140

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/833,823  
FILING DATE: 10-APR-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/514,014  
FILING DATE: 11-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A.  
REGISTRATION NUMBER: 32,724  
REFERENCE/DOCKET NUMBER: G16000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8224  
TELEFAX: (617) 876-5851

## INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:  
LENGTH: 153 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-833-823-12

## Query Match

Best Local Similarity 16.1%, Score 173; DB 2; Length 153;  
Matches 39; Conservative 16; Mismatches 31; Indels 14; Gaps 3;

QY 97 LEADTHOSISFWRYVDTEDEYPOKLAFAECLGCGIDARTGRTAALNSVRLQSL 156  
Db 60 MSRNIESRSTSPWNTYVTDPRYSEVVOACRNLGGINAO-GKEDISMSVPIQOETL 118

QY 157 VLRR--PCSRDSSGLPTGAFATFTEFHVPVGTCTVLP 194  
Db 119 VVRRKHQGS-----VSFOLEKVLTVVGTCTVLP 147

## RESULT 3

US-09-034-810-2  
Sequence 2, Application US/09034810  
Patent No. 6043344  
GENERAL INFORMATION:  
APPLICANT: Jacobs, Kenneth

APPLICANT: Kelleher, Kerry  
APPLICANT: Carlin, McKeough  
APPLICANT: Goldman, Samuel  
APPLICANT: Pittman, Debra  
APPLICANT: Mi, Sha  
APPLICANT: Neben, Steven  
APPLICANT: Giannotti, JoAnn  
APPLICANT: Golden/Fleet, Margaret

TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02140

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/034,810  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/685,239  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A.  
REGISTRATION NUMBER: 32,724  
REFERENCE/DOCKET NUMBER: G15262  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8224  
TELEFAX: (617) 876-5851

## INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
LENGTH: 163 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-034-810-2

## Query Match

Best Local Similarity 16.1%, Score 173; DB 3; Length 163;  
Matches 39; Conservative 16; Mismatches 31; Indels 14; Gaps 3;

QY 97 LEADTHOSISFWRYVDTEDEYPOKLAFAECLGCGIDARTGRTAALNSVRLQSL 156  
Db 70 MSRNIESRSTSPWNTYVTDPRYSEVVOACRNLGGINAO-GKEDISMSVPIQOETL 128

QY 157 VLRR--PCSRDSSGLPTGAFATFTEFHVPVGTCTVLP 194  
Db 129 VVRRKHQGS-----VSFOLEKVLTVVGTCTVLP 157

## RESULT 4

US-08-685-239-2  
Sequence 2, Application US/08685239  
Patent No. 6074849

GENERAL INFORMATION:  
APPLICANT: Jacobs, Kenneth  
APPLICANT: Kelleher, Kerry  
APPLICANT: Carlin, McKeough  
APPLICANT: Goldman, Samuel  
APPLICANT: Pittman, Debra  
APPLICANT: Mi, Sha  
APPLICANT: Neben, Steven  
APPLICANT: Giannotti, JoAnn  
APPLICANT: Golden/Fleet, Margaret  
TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins

NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/685,239  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A.  
REGISTRATION NUMBER: 32,724  
REFERENCE/DOCKET NUMBER: G15262  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8224  
TELEFAX: (617) 876-3851  
INFORMATION FOR SEQ ID NO.: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 163 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-685-239-2

Query Match 16.1%; Score 173; DB 3; Length 163;  
Best Local Similarity 39.0%; Pred. No. 1e-12; Indels 14; Gaps 3;  
Matches 39; Conservative 16; Mismatches 31;  
QY 97 LEADTHORSISPMRYVDDEDRYPQKLAFAECICRGCIDARTGRTAALNSVRLQSL 156  
DB 70 MERNIESRSTSPMNTVTMDPRNPSEVQACRNGCINAG-GKEDISMNSVP1QOETL 128  
QY 157 VLRR--PCSRDGSGLPTPGAFARFHTFIHVPGCTCVP 194  
DB 129 VVRKHGCS-----VSFOLEKVLVTVGCTCVP 157

RESULT 5  
US-08-620-694A-8  
Sequence 8, Application US/08620694A  
Patent No. 5869286  
GENERAL INFORMATION:  
APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, William  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 5869286e1 Receptor That Blinds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/620,694A  
FILING DATE: 21 MARCH 1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/538,765  
FILING DATE: 7 AUGUST 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO.: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 151 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Herpesvirus Saimiri  
STRAIN: ORF13  
US-08-620-694A-8

Query Match 15.0%; Score 160.5; DB 2; Length 151;  
Best Local Similarity 28.6%; Pred. No. 2.8e-11;  
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;  
QY 36 CYSAEELPIGOAAPHLLAGAKWGQALPVAVLSLEAASHRGHHERPSATTCQCPVLRPE 95  
DB 18 CYSSEITSAQTPRCIAA-----NSFPKSVMTTISIRMMNTSSKRA----- 60  
QY 96 VLEADTHORSISPMRYVDDEDRYPQKLAFAECICRGCIDARTGRTAALNSVRLQSL 155  
DB 61 ----DYNNSTSPWTLHRREDQDRYPSVIMEAKCRILGCVNA-DGVVDVHMNSVP1QOET 115  
QY 156 VLRR--PCSRDGSGLPTPGAFARFHTFIHVPGCTCVP 194  
DB 116 LVVRKHGQCPN-----SFRLEKMLVTVGCTCVP 145

RESULT 6  
US-09-034-810-6  
Sequence 6, Application US/09034810  
Patent No. 6043344  
GENERAL INFORMATION:  
APPLICANT: Jacobs, Kenneth  
APPLICANT: Kelleher, Kerry  
APPLICANT: Carlin, McKenough  
APPLICANT: Goldman, Samuel  
APPLICANT: Pittman, Debora  
APPLICANT: Mi, Sha  
APPLICANT: Neber, Steven  
APPLICANT: Giannotti, Johann  
TITLE OF INVENTION: Golden/Fleel, Margaret  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/034,810  
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/685,239

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

REFERENCE/DOCKET NUMBER: G12262

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 151 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-034-810-6

Query Match

Best Local Similarity 15.0%; Score 160.5; DB 3; Length 151;

Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

QY 36 CYSAEELPGQAPPHILARGAKWGQALPVALLVSSLEASHGHRHPRPATTCQVLRPEE 95

DB 18 CIVKSEITSAQIPRLCAA-----NNSPFRSVWVLTISTNNMTSSKRAS-----60

QY 96 VLEADTHORSTSPWRYRVDTEDEYPOKLAFAECICRCIDARTGRETAALNSVRLQSL 155

DB 61 ----DYKNSISPMWLNHNEQDRPSVIMWAKCRYLGCYVA--DGNVDYHNSVPIQGEI 115

QY 156 LVLR--RPGSRDGSGLPTPGAFAFHTFEIHPVGCCTCVP 194

DB 116 LVVRKHQPCPN-----SFRLEKMLVTVGCTCTVP 145

RESULT 7

US-09-022-255-8

Sequence 8, Application US/09022255

Patent No. 6072033

GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin

APPLICANT: Spriggs, Melanie

TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: Apple Power Macintosh

SOFTWARE: Microsoft Word for Apple, Version 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/022,255

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/620,694

FILING DATE: 21 MARCH 1996

APPLICATION NUMBER: USSN 08/538,765

FILING DATE: 7 AUGUST 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/410,535

APPLICATION NUMBER: USSN 08/410,535

FILING DATE: 23 MARCH 1995

ATTORNEY/AGENT INFORMATION:

NAME: Petkins, Patricia Anne

REGISTRATION NUMBER: 34,695

REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 151 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Herpesvirus Saimiri

STRAIN: ORF13

US-09-022-255-8

Query Match

Best Local Similarity 15.0%; Score 160.5; DB 3; Length 151;

Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

QY 36 CYSAEELPGQAPPHILARGAKWGQALPVALLVSSLEASHGHRHPRPATTCQVLRPEE 95

DB 18 CIVKSEITSAQIPRLCAA-----NNSPFRSVWVLTISTNNMTSSKRAS-----60

QY 96 VLEADTHORSTSPWRYRVDTEDEYPOKLAFAECICRCIDARTGRETAALNSVRLQSL 155

DB 61 ----DYKNSISPMWLNHNEQDRPSVIMWAKCRYLGCYVA--DGNVDYHNSVPIQGEI 115

QY 156 LVLR--RPGSRDGSGLPTPGAFAFHTFEIHPVGCCTCVP 194

DB 116 LVVRKHQPCPN-----SFRLEKMLVTVGCTCTVP 145

RESULT 8

US-09-022-696-8

Sequence 8, Application US/09022696

Patent No. 6072037

GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin

APPLICANT: Spriggs, Melanie

TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: Apple Power Macintosh

SOFTWARE: Microsoft Word for Apple, Version 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/022,696

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/620,694

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/410,535

FILING DATE: 23 MARCH 1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 151 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Herpesvirus Saimiri  
STRAIN: ORF13  
US-09-022-696-8

Query Match 15.0%; Score 160.5; DB 3; Length 151;  
Best Local Similarity 28.6%; Pred. No. 2.8e-11;  
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

QY 36 CYSAEELPLGQAPPHILARGAKWGALPVALVSSLEASHRGRHRRPSATTGCPVLRPE 95  
DB 18 CIVKSEITSAGTPRCIAA-----NNSFPRSVAVTLISIRWMTSSKRAS----- 60  
QY 96 VLEADTHORSISPMRYRYDDEDYRPOKLAFAECRCIDARTGRTAALNSVRLQSL 155  
DB 61 ----DYNNSTSPWTLHRNEDODRYPSYIWEAKCRYLGCVNA-DGVVDYHMNSVPIQGEI 115  
QY 156 LVLR--RPSGRDGSGLTPGAFATHTETIHVPVGTCTVLP 194  
DB 116 LVVRKGHQCPRN-----SFLRKLMLVTGCTCTVTP 145

RESULT 9  
US-08-685-239-6  
Sequence 6, Application US/08685239  
Patent No. 6074849  
GENERAL INFORMATION:  
APPLICANT: Jacobs, Kenneth  
APPLICANT: Kelleher, Kerry  
APPLICANT: Carlin, McKeough  
APPLICANT: Goldman, Samuel  
APPLICANT: Pittman, Debra  
APPLICANT: Mi, Sha  
APPLICANT: Neben, Steven  
APPLICANT: Giannotti, JoAnn  
APPLICANT: Golden/Pleee, Margaret  
TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/685,239  
FILING DATE:  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A.  
REGISTRATION NUMBER: 32,724  
REFERENCE/DOCKET NUMBER: G15262  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8224  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 151 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-685-239-6

Query Match 15.0%; Score 160.5; DB 3; Length 151;  
Best Local Similarity 28.6%; Pred. No. 2.8e-11;  
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

QY 36 CYSAEELPLGQAPPHILARGAKWGALPVALVSSLEASHRGRHRRPSATTGCPVLRPE 95  
DB 18 CIVKSEITSAGTPRCIAA-----NNSFPRSVAVTLISIRWMTSSKRAS----- 60  
QY 96 VLEADTHORSISPMRYRYDDEDYRPOKLAFAECRCIDARTGRTAALNSVRLQSL 155  
DB 61 ----DYNNSTSPWTLHRNEDODRYPSYIWEAKCRYLGCVNA-DGVVDYHMNSVPIQGEI 115  
QY 156 LVLR--RPSGRDGSGLTPGAFATHTETIHVPVGTCTVLP 194  
DB 116 LVVRKGHQCPRN-----SFLRKLMLVTGCTCTVTP 145

RESULT 10  
US-09-022-253-8  
Sequence 8, Application US/09022253  
Patent No. 6096305  
GENERAL INFORMATION:  
APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,253  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/620,694  
FILING DATE: 21-MARCH-1996  
APPLICATION NUMBER: USSN 08/538,765  
FILING DATE: 7 AUGUST 1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 151 amino acids  
TYPE: amino acid  
STRANDEDNESS: No. 6096305 Relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Herpesvirus Saimiri  
STRAIN: ORF13  
US-09-022-253-8

Query Match 15.0%, Score 160.5; DB 3; Length 151;  
Best Local Similarity 28.6%; Pred. No. 2.8e-11;  
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

QY 36 CYSAEELPLGQAPPHILARGAKWGQALPVAVSSLEASHRGHRRPSATTQCPVLRPEE 95  
DB 18 CIVKSEITSAQTPRCIAA-----NSFPRSVAVTILSRNMNTSSKRAS-----60  
QY 96 VLEADTHORSISPMRYRVDTDEDYPOKLAFAECICRCIDARTGRTAALNSVRLQSL 155  
DB 61 ----DYNNSTSPMTLHRNEDODRPSYIWEAKCRILGCVNA-DGNDVYHMSVFIQOEI 115  
QY 156 LVLR--RPSNRGSGSLPFGAFHTEFIHVPVCTCYLP 194  
DB 116 LVYRKGHQPCPN-----SFLEKMLVTGCTCTVP 145

RESULT 11  
US-09-022-260-8

Sequence 8, Application US/09022260  
Patent No. 6100235

GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,260  
FILING DATE:

CLASSIFICATION:

Prior Application DATA:

APPLICATION NUMBER: 08/620,694

FILING DATE:

CLASSIFICATION:

Prior Application DATA:

APPLICATION NUMBER: USSN 08/410,535

FILING DATE: 23 MARCH 1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 151 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Herpesvirus Saimiri  
STRAIN: ORF13  
US-09-022-260-8

Query Match 15.0%, Score 160.5; DB 3; Length 151;  
Best Local Similarity 28.6%; Pred. No. 2.8e-11;  
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

QY 36 CYSAEELPLGQAPPHILARGAKWGQALPVAVSSLEASHRGHRRPSATTQCPVLRPEE 95  
DB 18 CIVKSEITSAQTPRCIAA-----NSFPRSVAVTILSRNMNTSSKRAS-----60  
QY 96 VLEADTHORSISPMRYRVDTDEDYPOKLAFAECICRCIDARTGRTAALNSVRLQSL 155  
DB 61 ----DYNNSTSPMTLHRNEDODRPSYIWEAKCRILGCVNA-DGNDVYHMSVFIQOEI 115  
QY 156 LVLR--RPSNRGSGSLPFGAFHTEFIHVPVCTCYLP 194  
DB 116 LVYRKGHQPCPN-----SFLEKMLVTGCTCTVP 145

RESULT 12  
US-09-022-259-8

Sequence 8, Application US/09022259  
Patent No. 6191104

GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,259  
FILING DATE:

CLASSIFICATION:

Prior Application DATA:

APPLICATION NUMBER: 08/620,694

FILING DATE:

CLASSIFICATION:

Prior Application DATA:

APPLICATION NUMBER: USSN 08/410,535

FILING DATE: 23 MARCH 1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 151 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Herpesvirus Saimiri  
STRAIN: ORF13  
US-09-022-259-8

Query Match 15.0%; Score 160.5; DB 4; Length 151;  
Best Local Similarity 28.6%; Pred. No. 2.8e-11;  
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

QY 36 CYSAEELPLGQAPPHILARGAKWGQALPVALVSSLEAASHRGHRHPSATTCQPVLRPEE 95  
DB 18 CIVKSEITSAQIPRCIAA-----NNSFPRSVVTLIRMMNTSSKRAS-----60  
QY 96 VLEADTHOSISPMWRVDTDEDRYPQKLAFAECICRGIDARTGRTAALNSVRLQSL 155  
DB 61 ----DYNNSTSPWTLHRREDODRYPVWEAKCRYLGCVNA-DGNVDYHMNSVPIQDEI 115  
QY 156 LVLR--RPSCRDGSGLPTPGAFAFHTEFIHVPVCTCYP 194  
DB 116 LVVRKGHPCPN-----SFRLEKMLTVYGCTCYP 145

## RESULT 13

US-09-022-257-8  
Sequence 8, Application US/09022257  
Patent No. 6197525

## GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,257

## PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/620,694  
FILING DATE:

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995

## CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 151 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Herpesvirus Saimiri  
STRAIN: ORF13  
US-09-022-257-8

Query Match 15.0%; Score 160.5; DB 4; Length 151;  
Best Local Similarity 28.6%; Pred. No. 2.8e-11;  
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

QY 36 CYSAEELPLGQAPPHILARGAKWGQALPVALVSSLEAASHRGHRHPSATTCQPVLRPEE 95  
DB 18 CIVKSEITSAQIPRCIAA-----NNSFPRSVVTLIRMMNTSSKRAS-----60  
QY 96 VLEADTHOSISPMWRVDTDEDRYPQKLAFAECICRGIDARTGRTAALNSVRLQSL 155  
DB 61 ----DYNNSTSPWTLHRREDODRYPVWEAKCRYLGCVNA-DGNVDYHMNSVPIQDEI 115  
QY 156 LVLR--RPSCRDGSGLPTPGAFAFHTEFIHVPVCTCYP 194  
DB 116 LVVRKGHPCPN-----SFRLEKMLTVYGCTCYP 145

## RESULT 14

US-08-432-994A-4  
Sequence 4, Application US/08432994A  
Patent No. 6274711

## GENERAL INFORMATION:

APPLICANT: Golstein, Pierre  
APPLICANT: Rouvler, Eric  
APPLICANT: Fossiez, Francois  
APPLICANT: Lebecque, Serge J.E.  
APPLICANT: Djossou, Odile  
APPLICANT: Bancheureau, Jacques  
TITLE OF INVENTION: PURIFIED MAMMALIAN CTLA-8 ANTIGENS AND  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/432,994A  
FILING DATE: 02-MAY-1995

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/250,846  
FILING DATE: 27-MAY-1994

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/177,747  
FILING DATE: 05-JAN-1994  
APPLICATION NUMBER: US 08/077,203

FILING DATE: 14-JUN-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Chung, Edwin P.  
 REGISTRATION NUMBER: 34,090  
 REFERENCE/DOCKET NUMBER: DX0388K3  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-852-9196  
 TELEFAX: 415-496-1200  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 151 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-432-994A-4

Query Match 15.0%; Score 160.5; DB 4; Length 151;  
 Best Local Similarity 28.6%; Pred. No. 2.8e-11;  
 Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

QY 36 CTSAEPLPGQAPPHLLAAGAAWGAALPVATVSLFAASHRGHRHPSATTCQPLREE 95  
 DB 18 CIVKSEITSAQTPCLIA-----NNSPFRSVWVLTSTINMTSSKRAS-----60  
 QY 96 VLEADTHOSISPMRYRYDTEDEYPOKLAFAECRCGCDIARTGRETALNSVRLLOSL 155  
 DB 61 ----DYNRSTSPWNLHREDEPRYPVIMEAKCRHLGCTINA-DGWDVYHNSVPIQDEIIVL 115  
 QY 136 LVLR--RCSRSGSLPTPGAFAFHTEFIHVPVGTCTVLP 194  
 DB 116 LVRRKGHPCPN-----SFLRKMLVTVGCTCTVP 145

# RESULT 15

US-08-432-994A-8  
 Sequence 8, Application us/08432994A  
 Patent No. 6274711  
 GENERAL INFORMATION:  
 APPLICANT: Golstein, Pierre  
 APPLICANT: Rouvier, Eric  
 APPLICANT: Fossiez, Francois  
 APPLICANT: Lebecque, Serge J.E.  
 APPLICANT: Djossou, Odile  
 APPLICANT: Bancheureau, Jacques  
 TITLE OF INVENTION: PURIFIED MAMMALIAN CTLA-8 ANTIGENS AND  
 TITLE OF INVENTION: RELATED REAGENTS  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: DNAX Research Institute  
 STREET: 901 California Avenue  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94304-1104  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/432,994A  
 FILING DATE: 02-MAY-1995  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/250,846  
 FILING DATE: 27-MAY-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/177,747  
 FILING DATE: 05-JAN-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/077,203  
 FILING DATE: 14-JUN-1993

ATTORNEY/AGENT INFORMATION:  
 NAME: Chung, Edwin P.  
 REGISTRATION NUMBER: 34,090  
 REFERENCE/DOCKET NUMBER: DX0388K3  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-852-9196  
 TELEFAX: 415-496-1200  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 155 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-432-994A-8

Query Match 14.7%; Score 158; DB 4; Length 155;  
 Best Local Similarity 39.8%; Pred. No. 5.7e-11;  
 Matches 39; Conservative 11; Mismatches 34; Indels 14; Gaps 3;

QY 99 ADTHOSISPMRYRYDTEDEYPOKLAFAECRCGCDIARTGRETALNSVRLLOSLVL 158  
 DB 64 SDYNRSTSPWNLHREDEPRYPVIMEAKCRHLGCTINA-DGWDVYHNSVPIQDEIIVL 122  
 QY 159 RRRP--CSRSGSLPTPGAFAFHTEFIHVPVGTCTVLP 194  
 DB 123 RRRP--CSRSGSLPTPGAFAFHTEFIHVPVGTCTVLP 149

Search completed: September 4, 2002, 01:57:52  
 Job time: 314 sec







GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2002, 01:54:03 ; Search time 19.18 seconds

(without alignments)  
986.945 Million cell updates/sec

Title: US-09-854-280-3

Perfect score: 1073  
Sequence: 1 MTLPLGLLFTWLHTLAAHH.....FHTTEFIHVPVGTCTVLPKRV 197

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	160.5	15.0	151	1	BA5351
2	148.5	13.8	147	2	JC4628
3	148.5	13.8	150	2	I49623
4	110	10.3	148	2	T21334
5	93.5	8.7	395	1	KISM6
6	86.5	8.1	389	2	T50809
7	86	8.0	297	2	J10032
8	84.5	7.9	1638	2	A42091
9	82.5	7.7	635	2	S76371
10	81.5	7.6	325	2	T23218
11	81	7.5	553	2	D83640
12	80.5	7.5	210	2	B40203
13	80	7.5	411	2	A70509
14	79.5	7.4	638	2	UC7753
15	79	7.4	549	2	I37386
16	79	7.4	837	2	T12514
17	79	7.4	885	2	S75894
18	78.5	7.3	132	2	E72603
19	78	7.3	309	2	T37033
20	77.5	7.2	209	2	T30698
21	77.5	7.2	323	2	A35909
22	77.5	7.2	567	2	E96764
23	77	7.2	420	2	T14166
24	77	7.2	466	2	T36212
25	77	7.2	639	2	P97670
26	77	7.2	639	2	AC2895
27	76.5	7.1	405	2	G84338
28	76.5	7.1	503	2	S64787
29	76.5	7.1	1882	2	T00069

30	76	7.1	296	2	T35477	probable oxidoredu
31	75.5	7.0	1044	2	T00342	hypothetical prote
32	75	7.0	744	2	C75276	sensory box sensor
33	74.5	6.9	464	2	T50955	hypothetical prote
34	74.5	6.9	624	2	B49364	hypothetical prote
35	74	6.9	211	2	G72649	protein kinase (EC
36	74	6.9	260	1	A46517	hypothetical prote
37	74	6.9	347	2	JH0657	CD27 antigen precu
38	73.5	6.8	559	2	S33724	hypothetical 37.5k
39	73.5	6.8	741	2	I48694	transcription fact
40	73	6.8	329	2	T08262	probable transcript
41	73	6.8	373	2	B70673	hypothetical prote
42	73	6.8	1080	2	T43164	probable ddla - My
43	72.5	6.8	181	2	T24914	lacta protein - Li
44	72.5	6.8	362	2	B87571	hypothetical prote
45	72.5	6.8	466	2	A36389	hypothetical prote

## ALIGNMENTS

## RESULT 1

BA5351  
Immediate-early protein 2 - salmirline herpesvirus 1 (strain 11)

N:Alternate names: hypothetical protein ORF13  
C:Species: salmirline herpesvirus 1

A:Note: host Salmirl sciurus (common squirrel monkey)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Jul-1999

C:Accession: BA5351; D36807  
R:Nicholas, J.; Smith, E.P.; Coles, L.; Honess, R.

A:Title: Gene expression in cells infected with gammaherpesvirus salmirl: properties  
A:Reference number: A45351; MUID:91021021

A:Accession: BA5351  
A:Molecule type: mRNA

A:Residues: 1-151 <NIC>

A:Cross-references: GB:M60286; NID:9331040; PIDN:AAA46156.1; PID:9331042

R:Albrecht, J.  
A:Description: Primary structure of the herpesvirus salmirl genome..

A:Reference number: A36806  
A:Accession: D36807

A:Molecule type: DNA  
A:Residues: 1-151 <ALB>

A:Cross-references: GB:X64346; NID:960320; PIDN:CAA45636.1; PID:960334  
R:Albrecht, J.C.; Nicholas, J.; Biller, D.; Cameron, K.R.; Biesinger, B.; Newman, C.;

J. Virol. 66, 5047-5058, 1992  
A:Title: Primary structure of the herpesvirus salmirl genome.

A:Reference number: A37309; MUID:92333688  
A:Contents: annotation: protein-coding frames

A:Note: neither protein nor nucleotide sequence is given  
C:Genetics:

A:Gene: 13  
C:Superfamily: salmirl herpesvirus

A:Keywords: early protein immediate-early protein 2  
C:Keywords: early protein

Query Match: 15.0%; Score 160.5; DB 1; Length 151;  
Best Local Similarity 28.6%; Pred. No. 1.2e-07;  
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

QY	36	CYSAEELPLGQAPHLILAGAKMGQALPVALVSSLEAASHRGHRHERPSATTCQVLPRLPEE	95
DB	18	CIYKSEITSAQPPRCILAA-----NNSFPSSVATLISIRNMWTSKRAS-----	60
QY	96	VLEADTHORSISPMRYRVDTDEDYRPOKLAFCICRGCIDARTGRTAALNSVRLLOSL	155
DB	61	---DYNNSTSPWTLHRHEDDRPSYIWEAKKRTLCGVNA-DGAVDYMNSVPIQDEI	115
QY	156	LVLRR-RPCSRDGSGLPTPGAFAFHTFEFIHVPCTCTVLP	194
DB	116	LVRKRGHGPCPN-----SFLKMLVTVGCTCTVTP	145

## RESULT 2

JC4628  
 Cytotoxic T-lymphocyte-associated antigen 8 precursor - mouse  
 N:Alternate names: CTLA8 protein  
 C:Species: Mus musculus (house mouse)  
 C>Date: 10-May-1996 #sequence\_revision 19-Jul-1996 #text\_change 26-Aug-1999  
 C:Accession: JC4628  
 R:Yao, Z.; Timour, M.; Painter, S.; Fanslow, W.; Spilgus, M.  
 Gene 168, 223-225, 1996  
 A:Title: Complete nucleotide sequence of the mouse CTLA8 gene.  
 A:Reference number: JC4628; MUID:96194901  
 A:Accession: JC4628  
 A:Molecule type: DNA  
 A:Residues: 1-147 <YAO>  
 A:Cross-references: GB:U5108; NID:g1244499; PIDN:AAA93253.1; PID:g1244500  
 C:Genetics:  
 A:Gene: ctla8  
 A:Introns: 69/2  
 C:Superfamily: salm1r1 herpesvirus immediate-early protein 2  
 C:Keywords: cytokine; glycoprotein; lymphocyte  
 F:1-14/Domain: signal sequence #status predicted <SIG>  
 F:15-147/Product: cytotoxic T-lymphocyte-associated antigen 8 #status predicted <MAT>  
 F:60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 13.8%; Score 148.5; DB 2; Length 147;  
 Best Local Similarity 37.6%; Pred. No. 1.5e-06;  
 Matches 38; Conservative 13; Mismatches 35; Indels 15; Gaps 3;

QY 92 REEVLADTHQSTSPRYVDDEDRYPQKLAFAECLRGCDARTGRTAALNSVRL 151  
 DB 54 RPSDL-----NRSTSPMTLHNEDEDRYPVIMWAOGRHRCVNAE-GKLDHNMNSVLI 107

QY 152 LOSLLVLRRCPCSRDGLPTPGAFATFEFIHVPVCTCV 192  
 DB 108 QOEILVLRKEPS-----CPETFEVKMLVGVCTCV 139

## RESULT 3

149623  
 Cytotoxic T-lymphocyte-associated antigen 8 precursor - mouse  
 N:Alternate names: Immediate-early protein 2 (ORF13) homolog  
 C:Species: Mus musculus (house mouse)  
 C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 26-Aug-1999  
 C:Accession: 149623  
 R:Rouvier, E.; Luciani, M.  
 J: Immunol. 150, 5445-5456, 1993  
 A:Title: CTLA-8, cloned from an activated T cell, bearing AU-rich messenger RNA instability  
 A:Reference number: 149623; MUID:93294300  
 A:Accession: 149623  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-150 <RDS>  
 A:Cross-references: GB:U13839; NID:g293329; PIDN:AAA37490.1; PID:g293330  
 C:Genetics:  
 A:Gene: Ccla-8  
 C:Superfamily: salm1r1 herpesvirus immediate-early protein 2

Query Match 13.8%; Score 148.5; DB 2; Length 150;  
 Best Local Similarity 29.4%; Pred. No. 1.5e-06;  
 Matches 45; Conservative 20; Mismatches 55; Indels 33; Gaps 5;

QY 42 LPIGQAPPHILGAKMGALPVALVSSLEASHRGHRRSPSTTCCPVLRPEVEADT 101  
 DB 21 IPSSVCPNAENNFQNKVKIKYNSL---SSKASSRRPS-----DY 61

QY 102 HORSISPMRYVDDEDRYPQKLAFAECLRGCDARTGRTAALNSVRLGSLVLR 161  
 DB 62 LNRSTSPMTLHNEDEDRYPVIMWAOGRHRCVNAE-GKLDHNMNSVLIQOEILVLRKE 120

QY 162 P--CSRDSGLPTPGAFATFEFIHVPVCTCV 192

DB 121 PEKC-----PFTFEVKMLVGVCTCV 142

## RESULT 4

T21334  
 hypothetical protein F25D1.3 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T21334  
 R:Kelly, P.  
 submitted to the EMBL Data Library, June 1996  
 A:Reference number: Z19408  
 A:Accession: T21334  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-148 <ML>  
 A:Cross-references: EMBL:Z73973; PIDN:CAA98268.1; GSPDB:GN00023; CESP:F25D1.3  
 C:Genetics:  
 A:Gene: CESP:F25D1.3  
 A:Map position: 5  
 A:Introns: 60/2

Query Match 10.3%; Score 110; DB 2; Length 148;  
 Best Local Similarity 33.0%; Pred. No. 0.0054;  
 Matches 31; Conservative 17; Mismatches 34; Indels 12; Gaps 4;

QY 103 ORSISPMRYVDDEDRYPQKLAFAECLRGCDARTGRTAALNSVRLGSLVLR 162  
 DB 51 ERALCPWDSRVNVOERERKLIASVCLC-----RKSQSGACMCPVIRVPLIRVS 104

QY 163 CSRDSGLPTPGAFATFEFIHVPVCTCV 196  
 DB 105 CDR-STGL---WNYVSTELI--TVGCHSVLPRT 132

## RESULT 5

KISMG  
 galactokinase (EC 2.7.1.6) - Streptomyces sp.  
 C:Species: Streptomyces sp.  
 C>Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 28-May-1999  
 C:Accession: C28669  
 R:Adams, C.W.; Formwalt, J.A.; Schmidt, F.J.; Rosenberg, M.; Branner, M.E.  
 J: Bacteriol. 170, 203-212, 1988  
 A:Title: Gene organization and structure of the Streptomyces lividans gal operon.  
 A:Reference number: A28669; MUID:88086869  
 A:Accession: C28669  
 A:Molecule type: DNA  
 A:Residues: 1-395 <ADA>  
 A:Cross-references: GB:M18953; NID:g153259; PIDN:AAA26748.1; PID:g153262  
 A:Note: the source is designated as Streptomyces lividans  
 C:Genetics:  
 A:Gene: galK  
 A:Superfamily: galactokinase  
 C:Keywords: Arp; galactose metabolism; phosphotransferase

Query Match 8.7%; Score 93.5; DB 1; Length 395;  
 Best Local Similarity 29.3%; Pred. No. 0.53;  
 Matches 44; Conservative 15; Mismatches 79; Indels 11; Gaps 5;

QY 32 GTPHCYSAEELPLGAPPHILARG-AKW---GOALPVALVSSLEASHRGHRRSPSAT 86  
 DB 183 GTPSSVPATSPGSRSPSTSPRCACMSSTPGSSTPTAASARAARAPRCWAST 242

QY 87 QC--PVLRPEVEADTHQSTSPRYVDDEDRYPQKLAFAECLRGCDARTGRTA 144  
 DB 243 RCDVPYADLLAALERLDDEEVRRLVHVVTEDERVRVALLSAPGASAPSWSPATP 302

QY 145 ALNSVRLGSLVLRRCPCSRDGLPTPGAFATFEFIHVPVCTCV 173

Db 303 A---ARRLPRLP-RAGPGRHGRGRLGP 327

# RESULT 6

hypothetical protein T30N20\_270 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)  
C.Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 21-Jul-2000

C:Accession: T50809

R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Men  
Submitted to the Protein Sequence Database, July 2000

A:Reference number: Z25240

A:Accession: T50809

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-389 <BEV>

A:Cross-references: EMBL:AL365234

A:Experimental source: cultivar Columbia; BAC clone T30N20

C:Genetics:

A:Map position: 5

A:Note: T30N20\_270

Query Match 8.1%; Score 86.5; DB 2; Length 389;  
Best Local Similarity 23.0%; Pred. No. 2.3;  
Matches 56; Conservative 25; Mismatches 83; Indels 79; Gaps 10;

QY 6 GLLFLWLTCLAHNDPSLRGHP---HSHGTPICYSAEELPLGQAPP-HL-----LA----- 53

Db 44 GVEYLTWSRTFLGSHSVNLFHSQDYNNHSSPLSFSSADLSLSAVSFHLNLTNTLAFMKK 103

QY 54 RGAK-----WG-----QALPVALY-----SLEASHRGHRR 81

Db 104 RGRFSPKIQVWDLSKAKFDSGSEPRSGFYIAVVDGEMGLLVDSVKEAFAARKSKAK 163

QY 82 PSATTCPLVLRPEVLEADTHORSISPMWRYRVDTRRPOKLAFACLCRCIDAR--- 138

Db 164 PPTNPQALLRKHFVGA-----RVETTKARFGCKKREISIDCRVEDAKLCE 211

QY 139 -----TGRETALNSVRLQSLV---LRRRCRDSGSGLETPGAFAP 178

Db 212 SVDSKQVLIKRLRMKFRGNEKEVDGVHVOISMDVYNNLFSKSSGSGGGGSHAVFWF 271

QY 179 HTE 181

Db 272 RFE 274

# RESULT 7

hypothetical 31.7K protein (aphe region) - Streptomyces griseus

C:Species: Streptomyces griseus  
C.Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 22-Oct-1999

C:Accession: J10032

R:Heinzel, P.; Weiditzky, O.; Distler, J.; Plepersberg, W.

Arch. Microbiol. 150, 184-192, 1988

A:Title: A second streptomycin resistance gene from Streptomyces griseus codes for strep

A:Reference number: J10031; MUID:86339496

A:Accession: J10032

A:Molecule type: DNA

A:Residues: 1-297 <HEI>

A:Cross-references: GB:M37378; GB:X56876; NID:g153162; PIDN:AAA26701.1; PID:g153164

A:Experimental source: strain N2-3-11

A:Note: the function of the protein is unknown; the orf1 gene and aphe (streptomyces-3"-

C:Genetics:

A:Gene: orf1

C:Superfamily: Streptomyces griseus hypothetical 31.7K protein (aphe region)

Query Match 8.0%; Score 86; DB 2; Length 297;  
Best Local Similarity 27.4%; Pred. No. 1.9;  
Matches 40; Conservative 15; Mismatches 55; Indels 36; Gaps 7;

QY 48 PPHLLARGAKGQALPVAL-----VSSLEASH-----RGHERPSA-----TQO 87

Db 28 PSRLLLG--WMRRAPLVLDQLRSTARSSSEYVADSAVPPGRGEDQPGRGVRFNQ 85

QY 88 CPVLRPEVLEADTHORS-----ISPMWRYRVDTRRPOKLAFACLCRCIDARTGRET 143

Db 86 APLSRRETLGLDLDYDAVVVYLGPD-----GCGPDHPDDMTLVALLRLLDGRFGRET 141

QY 144 ALNLSVRLQSLVLRRCRDSGSG 169

Db 142 -----RVVTELVDDRRRLAPVNSG 161

# RESULT 8

transcription activator SNF2/SMT2 homolog brm - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C.Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 20-Sep-1999

C:Accession: A42091

R:Tamkun, J.W.; Deuring, R.; Scott, M.P.; Kissinger, M.; Pattatucci, A.M.; Kaufman, J

Cell 68, 561-572, 1992

A:Title: brhama: a regulator of Drosophila homeotic genes structurally related to the

A:Reference number: A42091; MUID:92154670

A:Accession: A42091

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1638 <TM>

A:Cross-references: GB:M65049; NID:g157011; PIDN:AAA19661.1; PID:g157012

A:Experimental source: Iso-1

A:Note: sequence extracted from NCBI backbone (NCBIN:82354, NCBIIP:82360)

C:Genetics:

A:Gene: FlyBase:brm

A:Cross-references: FlyBase:FBgn0000212

C:Superfamily: unassigned bromodomain proteins; bromodomain homology

C:Keywords: transcription regulation

F.1451-1506/Domain: bromodomain homology <BRO>

Query Match 7.9%; Score 84.5; DB 2; Length 1638;  
Best Local Similarity 22.2%; Pred. No. 17;  
Matches 42; Conservative 26; Mismatches 70; Indels 51; Gaps 8;

QY 22 PSLRGPHSHGPHRCYSAEELPLGQAPP---LLARGAKGQALPVALVSSLEASHRG 77

Db 52 PCAYGHPRMGRRP-----GGPRCHMHPRHOGHIFSGKGRHMGMP---PTGRNMSPTQT 104

QY 78 RHRRPSATTCPLVLR-----PEVLEADTH--QRSISPMWRYRVDTRRPOKLA 125

Db 105 HGMPPNAPTOPCIVSPGCPGPPRPERSSQENLHALORALDSMEKGLQEDPRYSQLLA 164

QY 126 FAECLCRCIDARTGRETALNSVRLQS---LLVLRRCRDSR----- 166

Db 165 -----MRATSKHQHLNGNOVNLRTQITAYRLLARKPKISWMOQALQAQOQPP 215

QY 167 GSGLPFGA 175

Db 216 GPPIGPGA 224

# RESULT 9

hypothetical protein - Synecocystis sp. (strain PCC 6803)

C:Species: Synecocystis sp.

A:Variety: PCC 6803

C.Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 20-Jun-2000

C:Accession: S76371

R:Kanamuro, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,

K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocys

S.

A:Reference number: S74322; MUID:97061201

A:Accession: S76371

A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-635 <XAN>  
A:Cross-references: EMBL:D64000; GB:AB001339; NID:g1001484; PIDN:BA10223.1; PID:g100159  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C:Superfamily: gida protein

Query Match 7.7%; Score 82.5; DB 2; Length 635;  
Best Local Similarity 24.2%; Pred. No. 9.2;  
Matches 44; Conservative 21; Mismatches 60; Indels 57; Gaps 8;

19 HHDSLRGHHSHGTHPCYSAEEL-----PLGAPPHLLARGAKWG--QA 61  
Db HLSPIYGGFIDSKGPRCPSEIDKIVFADKESHQIFIEPEGHDIPELYIGFSGLEPEN 326  
OY 62 LPALVSLSEASHRGHERPSATTCQPVLRPEVEADTHQRSISPMRYVDTEDEDRP 121  
Db 327 VOLAMLOTLPGLLEN-----CVMLRPAVAYEYDFLPAT-----OCYP 362  
OY 122 OKLA--FAECLRCGICDARTGRETAA-----LNSVRLIQ--SLIVLRRCPSDGSGL 170  
Db 363 SLMTKRVAGLFCAGQINGTGTGEAAAGLAVAGINARHCQKSLIF-----SREGSVL 417  
OY 171 PT 172  
Db 418 GT 419

## RESULT 10

T32218

hypothetical protein K02B12.1 -Caenorhabditis elegans

C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Feb-2000  
C:Accession: T32218  
R:Harriis, B.  
submitted to the EMBL Data Library, July 1996  
A:Reference number: Z19710  
A:Accession: T32218  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-525 <WILL>  
A:Cross-references: EMBL:Z75711; PIDN:CA800031.1; GSPDB:GN00019; CESP:K02B12.1  
A:Experimental source: clone K02B12  
C:Genetics:  
A:Gene: CESP:K02B12.1  
A:Map position: 1  
A:Introns: 155/2; 189/3; 234/3; 268/3  
A:Superfamily: transcription factor P1t-1; homeobox homology; POU domain homology  
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 7.6%; Score 81.5; DB 2; Length 325;  
Best Local Similarity 25.9%; Pred. No. 5.5;  
Matches 29; Conservative 14; Mismatches 54; Indels 15; Gaps 4;

OY 9 FLVWLHTCLAHHDPSLRGHHSHGTHPCYSAEELPLGAPPHLLARGAKWGALPVALVS 68  
Db 12 FODPHRPMUYOQPOLHFMLEPDHMAVPHLAQSLP-----PPHILITS-----TAAVA 59  
OY 69 SLEASHRGHERPSATTCQPVLR-PEVEADTHQRSISPM--RYRVDTDE 117  
Db 60 AATIASOSITINOTSVTSPSCQIKQEVERPEIIQRLMPMPMPAPVAFQSCDD 111

## RESULT 11

D83640

hypothetical protein PA0049 [imported] - Pseudomonas aeruginosa (strain PA01)  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: D83640  
R:Stover, C.K.; Pham, X.Q.; Ertvin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Badian, S.; Yian, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Ladbis, K.; Lim,

..Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa  
A:Reference number: A82950; MUID:20437337  
A:Accession: D83640  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-553 <STOS>  
A:Cross-references: GB:AE00444; GB:AE004091; NID:g9945863; PIDN:AA603439.1; GSPDB:GN  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA0049

Query Match 7.5%; Score 81; DB 2; Length 553;  
Best Local Similarity 24.2%; Pred. No. 11;  
Matches 55; Conservative 16; Mismatches 72; Indels 84; Gaps 13;

OY 12 WLHTCLAHHDPSLRGHHSHGTHPCYSAEELP-----LQAPPHLLARG----- 55  
Db 305 WLEAMNGRFHGSAG--NDGIYCPADSALPNVPLPGSVTPGTAPISLRSGCINP 361  
OY 56 -----AKGQALPVAVSS-----LEASHRGHERPSATTCQPVLRPEVELE 98  
Db 362 PRRLGYDASARMQNLPAPFSKASLPYRLADLADTRKGLERPGATSOA-----AEGFD 416  
OY 99 ADTHORSISPMRYVDTEDEDRYPOKLAFAECLRCGICDARTGRETALNSV--RLIOSLL 156  
Db 417 VTWH-----TNDVDFPD-----CANRT--ENVPTGVNMMAMPDSL 451  
OY 157 VL-----RRRPSRDGSG--LPTGAF-----AFHEF-----IHVY 187  
Db 452 VLDPNRRICARNGCGDYLNSESAIVNTVLRDAFRLIEPAGHIVPV 498

## RESULT 12

B40203

4-alpha-glucanotransferase (EC 2.4.1.25) / amylo-1,6-glucosidase (EC 3.2.1.33) - pig

C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 28-Aug-1992 #sequence\_revision 28-Aug-1992 #text\_change 31-Mar-2000  
C:Accession: B40203  
R:Yang, B.Z.; Ding, J.H.; Engchild, J.J.; Bao, Y.; Chen, Y.T.  
J. Biol. Chem. 267, 9294-9299, 1992  
A:Title: Molecular cloning and nucleotide sequence of cDNA encoding human muscle glyc  
A:Reference number: A40203; MUID:92250533  
A:Accession: B40203  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-210 <YAN>  
A:Superfamily: 4-alpha-glucanotransferase / amylo-1,6-glucosidase  
C:Keywords: glycosidase; glycosyltransferase; hexosyltransferase; hydrolase; polysac

Query Match 7.5%; Score 80.5; DB 2; Length 210;  
Best Local Similarity 25.3%; Pred. No. 4.2;  
Matches 50; Conservative 17; Mismatches 76; Indels 55; Gaps 10;

OY 22 PSIRGHPHSHGT--PHGYS-AEELPLG---QAPPHLLARGAKWGQALPVALVSLEASH 75  
Db 3 PTLQCKPTVTVTNTPSCYSLADOLELNDPSRPK-----KENMLCITDVVYHTTANS 57  
OY 76 RGRHERPSAT-----TQCPVLRPEEV---LEADTHQRSISPMRYVDTEDE 118  
Db 58 RWLHEHPECAVNLVNSPHKALMHLSCDVAEGRGVPAALIENDHMSI-----RLTIWED 112  
OY 119 RYPOKLAFAECLRCGICDARTGRETALNSVRLIOSLLVLRRCPSDGSGLPTP----- 173  
Db 113 ITPKELLQWGDQVQAVDA-----LPSSTIV--SMACCSGSGTKNNPAASPS 157  
OY 174 --GAFAHTEFTHVPVC 189  
Db 158 DTGEVNFOSGITIEVPVC 175







GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2002, 01:56:43 ; Search time 10.9 Seconds  
(without alignments)  
699.794 Million cell updates/sec

Title: US-09-854-280-3

Perfect score: 1073  
Sequence: 1 MTLPLGLLFTWLHTCLAHH.....FHTFEIHPVGCCTCVLPRSV 197

Scoring table: BIOSIM62  
Gapop-10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues  
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1073	100.0	197	117C_HUMAN	O9P0M4 homo sapien
2	173	18.1	153	117F_HUMAN	O96PD4 homo sapien
3	168.5	15.7	180	117B_MOUSE	O94XT6 mus musculu
4	165.5	15.4	177	117E_HUMAN	O9H293 homo sapien
5	160.5	15.0	151	VG13_HSVSA	P24916 herpesvirus
6	158	14.7	155	1117_HUMAN	O16552 homo sapien
7	157.5	14.7	151	VG13_HSVSC	O40833 herpesvirus
8	157.5	14.7	178	117B_MESAU	O9EQ16 mesocricetu
9	154.5	14.4	180	117B_HUMAN	O9UH15 homo sapien
10	148.5	13.8	150	1117_RAT	O61453 rattus norv
11	148.5	13.8	158	1117_MOUSE	O62386 mus musculu
12	85.5	8.0	465	HNF6_HUMAN	O9UBC0 homo sapien
13	85.5	8.0	465	HNF6_MOUSE	O08755 mus musculu
14	85.5	8.0	465	HNF6_RAT	P70512 rattus norv
15	84.5	7.9	1638	BRM_DROME	P23439 drosophila
16	82.5	7.7	635	GIDA_SYNY3	O55694 synecocyst
17	81.5	7.6	325	HM06_CAEEL	P20268 caenorhabdi
18	79	7.4	549	FAST_HUMAN	O14296 homo sapien
19	77.5	7.2	323	FR42_CHICK	P18625 gallus galli
20	77.5	7.2	581	TR14_HUMAN	O15650 homo sapien
21	76.5	7.1	503	PR19_YEAST	P33523 saccharomyc
22	74.5	6.9	639	DMK_HUMAN	O09013 homo sapien
23	74	6.9	260	TNR7_HUMAN	P26842 homo sapien
24	74	6.9	976	EPAL_HUMAN	P21709 homo sapien
25	74	6.9	2842	ARC_RAT	P70478 rattus norv
26	73.5	6.8	559	HNF6_PIG	O03365 sus scrofa
27	73.5	6.8	741	NFL1_MOUSE	O61985 mus musculu
28	73	6.8	373	DDL_MYCTU	P95114 mycobacteri
29	72.5	6.8	466	GAT2_CHICK	P23824 gallus galli
30	72.5	6.8	528	CP15_CHICK	P79761 gallus galli
31	72.5	6.8	772	NFL1_HUMAN	O14494 h nuclear f
32	71.5	6.7	203	COBC_ECOLI	P52086 escherichia
33	71.5	6.7	214	VEGA_CANFA	O9MYV3 canis famli

## ALIGNMENTS

34	71.5	6.7	297	1	HXAB_CHICK	P31258 gallus galli
35	71.5	6.7	433	1	PMBE_ERMCH	O47474 erwina chr
36	71	6.6	322	1	FOS_AYINC	P23050 avian retro
37	71	6.6	342	1	CRTB_STRGR	P54977 streptomyc
38	71	6.6	367	1	FOS_CHICK	P11939 gallus galli
39	71	6.6	2564	1	SPCQ_HUMAN	O9H254 homo sapien
40	70.5	6.6	256	1	KPFA_AERPE	O9YF55 aeropyrum p
41	70.5	6.6	313	1	HXAB_MOUSE	P31311 mus musculu
42	70.5	6.6	705	1	PIXB_MOUSE	O96528 mus musculu
43	70	6.5	381	1	SEIP_MOUSE	P48908 homo sapien
44	70	6.5	411	1	HGX3_BRATL	P50901 branchiosto
45	70	6.5	839	1	ZF93_HUMAN	O9Y218 homo sapien

RESULT 1  
ID 117C\_HUMAN STANDARD: PRT: 197 AA.  
AC O9P0M4: O9HC75:  
DT 01-MAR-2002 (Rel. 41, Created)  
DT 01-MAR-2002 (Rel. 41, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Interleukin-17C precursor (IL-17C) (Cytokine CX2).  
GN IL17C.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20105548; PubMed=10639155;  
RA Li H., Chen J., Huang A., Stinson J., Heldens S., Foster J., Dowd P.,  
RA Gurney A.L., Wood W.L.;  
RT "Cloning and characterization of IL-17B and IL-17C, two new members  
RT of the IL-17 cytokine family.";  
RL Proc. Natl. Acad. Sci. U.S.A. 97:773-778(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Zhang W., He L., Wan T., Yuan Z., Gao X.;  
RT "Novel human cytokine CX2 with homology to IL-17.";  
RT Submitted (Apr-1999) to the EMBL/Genbank/DBJ databases.  
CC - FUNCTION: Stimulates the release of tumor necrosis factor alpha  
CC and IL-1beta from the monocytic cell line THP-1.  
CC - SUBCELLULAR LOCATION: Secreted.  
CC - SIMILARITY: BELONGS TO THE IL-17 FAMILY.  
CC -----  
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CC -----  
DR EMBL: AF152099; AAF28105.1; -;  
DR EMBL: AF142410; AAG27921.1; -;  
DR MIM: 604628; -;  
KW Cytokine; Signal.  
FT SIGNAL 1 18 POTENTIAL.  
FT CHAIN 19 197 INTERLEUKIN-17C.  
FT DISULFID 129 189 BY SIMILARITY.  
FT DISULFID 134 191 BY SIMILARITY.  
FT CONFLICT 50 50 H -> R (IN REF. 2).  
SQ SEQUENCE 197 AA; 21765 MW; BAE0152E18DE7D08 CRC64;  
Query Match 100.0%; Score 1073; DB 1; Length 197;  
Best Local Similarity 100.0%; Pred. No. 5.4e-94;  
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MTLPLGLLFTWLHTCLAHHPSLRNGHPHSHGTPHCYSAEELPLGQAPPHLARGAKWQ 60

```

Db 1 MTLLGLFETLMTCLAHDPSSLRGHPHSHGTPHCYSABELPLGQAPPLLAGKMGQ 60
OY 61 ALPALVSSLEASHRGRHREPPSATTOCPVLRPEVELEATHORSISPMRYDDEDEY 120
Db 61 ALPALVSSLEASHRGRHREPPSATTOCPVLRPEVELEATHORSISPMRYDDEDEY 120
OY 121 POKLAFAECRCGICDARTGRTETALNSVLLQSLVLRPPCSRDGSLPTPGAFAPFT 180
Db 121 POKLAFAECRCGICDARTGRTETALNSVLLQSLVLRPPCSRDGSLPTPGAFAPFT 180
OY 181 EFTHVPGCTCVLPRESV 197
Db 181 EFTHVPGCTCVLPRESV 197

RESULT 2
ID 117F_HUMAN STANDARD: PRT: 153 AA.
AC 096PD4; 09NUE6; 096P18;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE Interleukin-17F precursor (IL-17F) (Interleukin-24) (Cytokine ML-1)
GN IL17F OR IL24.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21475830; PubMed=11591732;
RA Starnes T., Robertson M.J., Siedge G., Kelich S., Nakshatri H.,
RA Broxmeyer H.E., Hromas R.,
RT "IL-17F, a novel cytokine selectively expressed in activated T cells
RT and monocytes, regulates angiogenesis and endothelial cell cytokine
RT production."
RT J. Immunol. 167:4137-4140(2001).
RN [2]
RP SEQUENCE OF 2-153 FROM N.A.
RA MEDLINE=21475866; PubMed=11591766;
RA Kawaguchi M., Onuchi L.F., Li X.-D., Essayan D.M., Schroeder J.,
RA Xiao H.-Q., Liu M.C., Krishnaswamy G., Germing G., Huang S.-K.,
RT "Identification of a novel cytokine, ML-1, and its expression in
RT subjects with asthma."
RT J. Immunol. 167:4430-4435(2001).
RN [3]
RP SEQUENCE OF 76-153 FROM N.A.
RA Almeida J.;
RN Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS), AND CHARACTERIZATION
RN PubMed=11574464;
RA Hymowitz S.G., Filvaroff E.H., Yin J.P., Lee J., Cai L., Risser P.,
RA Maruoka M., Mao W., Foster J., Kelley R.F., Pan G., Gurney A.L.,
RA de Vos A.M., Starovasnik M.A.,
RT "IL-17s adopt a cystine knot fold: structure and activity of a novel
RT cytokine, IL-17F, and implications for receptor binding."
RT EMBO J. 20:5332-5341(2001).
RN [5]
RP FUNCTION: Stimulates the production of other cytokines such as IL-
RN 6, IL-8 and granulocyte colony-stimulating factor, and can
RN regulate cartilage matrix turnover. Stimulates PBMC and T-cell
RN proliferation. Inhibits angiogenesis.
RN [6]
RP SUBUNIT: Homodimer; disulfide-linked.
RN [7]
RP TISSUE SPECIFICITY: Expressed in activated, but not resting, CD4+
RN T cells and activated monocytes.
RN [8]
RP SIMILARITY: BELONGS TO THE IL-17 FAMILY.
RN [9]
RP This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF384857; AAK83350.1; ALT_INIT.
DR EMBL: AF332389; AAL14427.1; ALT_INIT.
DR EMBL: AL034343; CAB75300.1;
DR MIM: 606496;
DR PDB: 1jpy; 28-SEP-01.
KW Cytokine; glycoprotein; signal; 3D-structure.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 153 INTERLEUKIN-17F.
FT CARBOHYD 73 73 N-LINKED (GLCNAC...).
FT DISULFID 37 37 INTERCHAIN (WITH C-127').
FT DISULFID 92 142
FT DISULFID 97 144
FT DISULFID 127 127
SO SEQUENCE 153 AA; 17009 MW; BA489BED83D57CE CRC64;

```

```

Query Match 16.1%; Score 173; DB 1; Length 153;
Best Local Similarity 39.0%; Pred. No. 1.7e-09;
Matches 39; Conservative 16; Mismatches 31; Indels 14; Gaps 3;

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OY 97 LEADTHORSISPMRYVDDEDEYPOKLAFAECRCGICDARTGRTETALNSVLLQSL 156
Db 60 MSNRISRSISPMRYVVDDEDEYPOKLAFAECRCGICDARTGRTETALNSVLLQSL 118
OY 157 VLNR--PCSRDGSGLPTPGAFAPFTFTHVPGCTCVLP 194
Db 119 VVRRKHQGS-----VSFLEKVLTVVGTCTVTP 147

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RESULT 3
ID 117B_MOUSE STANDARD: PRT: 180 AA.
AC 09OXT6; 099MY3; 09CT14;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Interleukin-17B precursor (IL-17B) (Cytokine-like protein ZCYT07)
DE (Neuronal Interleukin-17 related factor) (Cytokine CX1).
GN IL17B OR ZCYT07 OR N1RF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J.,
RA Martinez T., Hoffman R., O'Hara P.;
RN Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Moore E.E., Prenell S., Garrigues U., Guilbot A., Leguern E.,
RA Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.;
RT "Identification of a novel IL-17 related factor: demonstration of
RT neutral expression and evaluation as a candidate for the chromosome
RT 5q-linked form of Charcot-Marie-Tooth disease."
RN Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN=BALB/c;
RC Zhang W., Cao X.;
RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shtingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Atakawa T., Hara A., Fukunishi Y., Kono H., Aachii J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamazaki I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

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RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Glassl C., King B., Kochiwa H.,  
 RA Kuentz P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boileau D., Bojunga N., Carninci P., de Bonaldi M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamaya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasak H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
 RA Hayashizaki Y.,  
 RA \*Functional annotation of a full-length mouse cDNA collection.\*;  
 RT Nature 409:685-690(2001).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Strusberg R.,  
 RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: Stimulates the release of tumor necrosis factor alpha  
 CC and IL-1beta from the monocytic cell line THP-1 (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 DR EMBL: AF184970; AAF01319.1; -  
 DR EMBL: AF218726; AAC44135.1; -  
 DR EMBL: AF250308; AAK37427.1; -  
 DR EMBL: AK003506; BAB22826.1; -  
 DR EMBL: BC002271; AAH02271.1; -  
 DR MGI: 1928397; I117b.  
 KW Cytokine; Glycoprotein; Signal.  
 FT SIGNAL 1 22  
 FT CHAIN 23 180  
 FT DISULFID 121 176  
 FT DISULFID 126 178  
 FT CARBOHYD 75 75  
 FT CONFLICT 1 33  
 FT CONFLICT 34 34  
 FT CONFLICT 65 65  
 FT CONFLICT 76 76  
 FT SEQUENCE 180 AA; 20309 MW; E26F4C72001997C5 CRC64;  
 Query Match 15.7%; Score 168.5; DB 1; Length 180;  
 Best Local Similarity 27.0%; Pred. No. 5.5e-09;  
 Matches 53; Conservative 28; Mismatches 82; Indels 33; Gaps 6;  
 QY 7 LLELTLMTHTCLA-HHDSLRGHHSHGTPHCYSAEELPLGQAPPHLLARAKMGQALPVA 65  
 DB 7 LLELTLMTHTCLA-HHDSLRGHHSHGTPHCYSAEELPLGQAPPHLLARAKMGQALPVA 65  
 QY 66 LVSLSLAASHRGHRRSPATTCPLRPEVLEAD-----THORSISPMRYRDTD 116  
 DB 49 LVSRLVRYAMEYERLGMVAOLNRSSSPARKKCEVNIQLMLSNKRSLSPMGYSINHD 108  
 QY 117 EDRYPKLAFAECLRCGCIIDARTGRETALNSVRLQSLVLRRRPGRDGLPTPGAP 176  
 DB 109 PSRIPIADLPARCLICGCVNPFMTQEDRSKSVYVVF-SQVPRRRLCPGP-----PRGPGC 163  
 QY 177 AFTTEFLHVPVGCVCV 192  
 DB 164 RORVMTTAVGCTCI 179

RESULT 4  
 ID 117E.HUMAN STANDARD; PRT; 177 AA.  
 AC 09H293;  
 DT 01-MAR-2002 (Rel. 41, Created)  
 DT 01-MAR-2002 (Rel. 41, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Interleukin-17E precursor (IL-17E).  
 GN IL17E.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21125711; PubMed=11058597;  
 RA Lee J., Ho W.-H., Maruoka M., Corpuz R.T., Baldwin D.T., Foster J.S.,  
 RA Goddard A.D., Yansura D.G., Vandlen R.L., Wood W.I., Gurney A.L.,  
 RT IL-17E, a novel proinflammatory ligand for the IL-17 receptor homolog  
 RT IL-17Rb1.  
 RL J. Biol. Chem. 276:1660-1664(2001)  
 CC -1- FUNCTION: Induces activation of NF-kappaB and stimulates  
 CC production of the proinflammatory chemokine IL-8.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed at low levels in several tissues,  
 CC including brain, kidney, lung, prostate, testis, spinal cord,  
 CC adrenal gland, and trachea.  
 CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 DR EMBL: AF305200; AAG40848.1; -  
 DR MIM: 605658;  
 KW Cytokine; Glycoprotein; Signal.  
 FT SIGNAL 1 32  
 FT CHAIN 33 177  
 FT DISULFID 110 168  
 FT DISULFID 115 170  
 FT CARBOHYD 136 136  
 FT SEQUENCE 177 AA; 20330 MW; 52D895710CD59871 CRC64;  
 Query Match 15.4%; Score 165.5; DB 1; Length 177;  
 Best Local Similarity 29.7%; Pred. No. 1e-08;  
 Matches 52; Conservative 16; Mismatches 70; Indels 37; Gaps 7;  
 QY 27 HPHSHGTPHCYS-----AEELPLGQAPPHLLARAKMGQALPVVLSLEASHRGHRR 81  
 DB 31 HTYSHWSPSCPCSGQDPSSEL-----LRW-STVP---VPLRPAPRRHPHS 73  
 QY 82 PSATTCQPVLRPEVLEADTHORSISPMRYRVDTERYQKLAFAECLRCGCIIDARTG 141  
 DB 74 CRASEDGPL-----NSRAISPMRYELDRDLRPLDLYHARCLCPHCVSLOTGS 122  
 QY 142 ETAAL-NSVRLQSLVLRRRPGRDGLPTPGAFHFHEFLHVPVGCVCVPR 195  
 DB 123 HMDPRGNSLLYNQVYFTRPCHEGNG---TIKGYCLERRLRYVSLACVCPRR 174  
 RESULT 5  
 ID VG13.HSVSA STANDARD; PRT; 151 AA.  
 AC P24916;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Immediate early gene 13 protein precursor.  
 GN 13 OR KCLF2.  
 OS Herpesvirus saimiri (strain 11).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Gammaherpesvirinae; Rhadinovirus.  
 OX NCBI\_TaxID=10383;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90163221; PubMed=2154888;  
 RA Albrecht J.-C., Fleckenstein B.,  
 RT "Structural organization of the conserved gene block of Herpesvirus  
 saimiri coding for DNA polymerase, glycoprotein B, and major DNA  
 binding protein."  
 RL Virology 174:533-542(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92333688; PubMed=1321287;  
 RA Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger B.,  
 RA Newman C., Wiltmann S., Craxton M.A., Coleman H., Fleckenstein B.,  
 RA Honess R.W.,  
 RT "Primary structure of the herpesvirus saimiri genome."  
 RL J. Virol. 66:5047-5058(1992).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91021021; PubMed=1699352;  
 RA Nicholas J., Smith E.P., Coles L., Honess R.,  
 RT "Gene expression in cells infected with gammaherpesvirus saimiri:  
 properties of transcripts from two immediate-early genes."  
 RL Virology 179:189-200(1990).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.  
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DR EMBL: X63346; CAA45636.1;  
 DR EMBL: M31122; AAA46169.1;  
 DR EMBL: M60286; AAA46156.1;  
 DR PIR: D36807; D36807.  
 DR PIR: B45351; B45351.  
 KW Cytokine; Early protein; Signal.  
 FT CHAIN 1 22  
 FT SIGNAL 1 22  
 FT DISULFID 23 151  
 FT DISULFID 90 140  
 FT CARBOHYD 36 142  
 FT CARBOHYD 53 36  
 FT CARBOHYD 53 36  
 FT CARBOHYD 64 64  
 SQ SEQUENCE 151 AA; 17180 MW; 53BDD4206C432 CRC64;

Query Match 15.0%; Score 160.5; DB 1; Length 151;  
 Best Local Similarity 28.6%; Pred. No. 2.6e-08;  
 Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

QY 36 CYSAEELPGOAPPHLLGAKGALPVALLYSLEAASHRGRHERPSATTCOPVLRPEE 95  
 DB 18 CIYKSETTSKQTPRCIAA-----NSFPRSVVVTLSIRMMNTSSKRAS----- 60  
 QY 96 VLEADTHORSISFWRVYDDEDRYPQKLAFAECRCGIDARTGRFETALNSVRLQSL 155  
 DB 61 ----DYNNSTSPWTLHRNEDDRIPSVIWEAKCRILGCVN--DENVDYHNNSVIQQEIT 115  
 QY 156 LVLR--RCSRDGSLPTPGAFAFHTFRIHVPVGCCTVLP 194  
 DB 116 LVVRKGHPCPN-----SFLERKMLVTGCTCTVP 145

RESULT 6  
 ID IL17\_HUMAN  
 AC Q16552;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Interleukin-17 precursor (IL-17) (IL-17A) (Cytotoxic T lymphocyte-  
 associated antigen 8) (CTLA-8).  
 OS IL17 OR IL17A OR CTLA8.  
 GN Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96281911; PubMed=8676080;  
 RA Fossiez F., Djossou O., Chomarat P., Flores-Romo L., Alt-Yahia S.,  
 RA Mat C., Pin J.-J., Garrone P., Garcia E., Saeleand S., Blanchard P.,  
 RA Gaillard C., Das Mahapatra B., Rouvier E., Golstein P., Banchereau J.,  
 RA Lebecque S.;  
 RT "T cell interleukin-17 induces stromal cells to produce  
 RT proinflammatory and hematopoietic cytokines."  
 RL J. Exp. Med. 183:2593-2603(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=T-cell;  
 RX MEDLINE=96094436; PubMed=7499828;  
 RA Yao Z., Painter S.L., Fanslow W.C., Ulrich D., Macduff B.M.,  
 RA Spriggs M.K., Arncliffe R.J.;  
 RT "Human IL-17: a novel cytokine derived from T cells."  
 RL J. Immunol. 155:5483-5486(1995).  
 CC -1- FUNCTION: INDUCES STROMAL CELLS TO PRODUCE PROINFLAMMATORY AND  
 CC HEMATOPOIETIC CYTOKINES. ENHANCES THE SURFACE EXPRESSION OF THE  
 CC INTRACELLULAR ADHESION MOLECULE-1 (ICAM-1) IN FIBROBLASTS.  
 CC -1- SUBUNIT: HOMODIMER.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: RESTRICTED TO ACTIVATED MEMORY T-CELLS.  
 CC -1- PIM: FOUND BOTH IN GLYCOSYLATED AND NONGLYCOSYLATED FORMS.  
 CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.  
 CC -1- DATABASE: NAME=R&D Systems' cytokine mini-reviews: IL17;  
 CC WWW="http://www.rndsystems.com/asp/g\_sitbuilder.asp?bodyid=211".  
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DR EMBL: Z58820; CAA91233.1;  
 DR EMBL: U32659; AAC50341.1;  
 DR MIM: 603149;  
 KW Cytokine; Glycoprotein; T-cell; Antigen; Signal.  
 FT SIGNAL 1 23  
 FT CHAIN 1 23  
 FT DISULFID 24 155  
 FT DISULFID 94 144  
 FT DISULFID 99 146  
 FT CARBOHYD 68 68  
 SQ SEQUENCE 155 AA; 17504 MW; 28CAE9CB2F4886D1 CRC64;

Query Match 14.7%; Score 158; DB 1; Length 155;  
 Best Local Similarity 39.8%; Pred. No. 4.5e-08;  
 Matches 39; Conservative 11; Mismatches 34; Indels 14; Gaps 3;

QY 99 ADTHORSISFWRVYDDEDRYPQKLAFAECRCGIDARTGRFETALNSVRLQSL 158.  
 DB 64 SDYNNRSTSPWTLHRNEDDRIPSVIWEAKCRILGCVN--DENVDYHNNSVIQQEIT 122  
 QY 159 RRRP--CSRDSGLPTPGAFAFHTFRIHVPVGCCTVLP 194

DB 123 RREPCHPN-----SFLRKLTVSGCTCVP 149

RESULT 7

VG13\_HSVSC STANDARD; PRT; 151 AA.

AC 040633;

DT 01-MAR-2002 (Rel. 41, Created)

DT 01-MAR-2002 (Rel. 41, Last sequence update)

DE Immediate early gene 13 protein precursor.

OS Herpesvirus saimiri (subgroup C / strain 488).

OC Viruses: dsDNA viruses, no RNA stage; Herpesviridae;

OC Gammaherpesvirinae; Rhadinovirus.

OX NCBI\_TaxID=10384;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=98037620; PubMed=9371569;

RA Knappe A., Hiller C., Thurnau M., Wittmann S., Hofmann H.,

RA Fleckenstein B., Fieckenscher H.;

RT "The superantigen-homologous viral immediate-early gene iel4/vsag in

RT herpesvirus saimiri-transformed human T cells.;"

RL J. Virol. 71:9124-9133(1997).

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.

CC -----

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CC -----

DR EMBL: Y13183; CAA73627.1; -

KW Cytokine; Early protein; Signal.

FT SIGNAL 1 22

FT CHAIN 23 151 IMMEDIATE EARLY GENE 13 PROTEIN.

FT DISULFID 90 140 BY SIMILARITY.

FT DISULFID 95 142 BY SIMILARITY.

FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).

SO SEQUENCE 151 AA; 17189 MW; 49B2C9430C46BE32 CRC64;

Query Match 14.7%; Score 157.5; DB 1; Length 151;

Best Local Similarity 28.6%; Pred. No. 4.9e-08;

Matches 46; Conservative 22; Mismatches 58; Indels 35; Gaps 5;

OY 36 CYSAEELPLPGAPPHLLANGAKWGQALPVALLSSLEASHRGHRRPSATTQCPVLRPEE 95

DB 18 CIVKSTSTSAQTPRLIA-----NNSFPRSVVLTLSIRNMNTSSKRAS----- 60

OY 96 VLEADPHOSISPMWRVDTDEDRYPQKLAFAECLRCGIDARTGRTALNSVRLQSL 155

DB 61 ----DYNSTSPWLYRNEDDPRPSVWEAKCRYLGVNA-DGNVDYHMNSVPLODEI 115

OY 156 LVLR--RPRCSRDSGLPTPGAFAFHTEFIHVPVGCCTVLP 194

DB 116 LVVRKGNHNCPP-----SFLRKLMTVYGCCTCVP 145

RESULT 8

117B\_MESAU

ID 117B\_MESAU STANDARD; PRT; 178 AA.

AC 09E016;

DT 01-MAR-2002 (Rel. 41, Created)

DT 01-MAR-2002 (Rel. 41, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Interleukin-17 precursor (IL-17B) (Neuronal Interleukin-17 related factor) (Fragment).

GN IL17B OR N1RF.

OS Mesocricetus auratus (Golden hamster).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;

OC Mesocricetus.

OX NCBI\_TaxID=10036;

RN [1]

RP SEQUENCE FROM N.A.

RA Moore E.E., Presnell S., Garrigue U., Guilhot A., LeGuern E.,

RA Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.;

RT "Identification of a novel IL-17 related factor: demonstration of

RT neuronal expression and evaluation as a candidate for the chromosome

RT 5q-linked form of Charcot-Marie-Tooth disease.;"

RL Sg-linked form of Charcot-Marie-Tooth disease.;"

CC -1- FUNCTION: Stimulates the release of tumor necrosis factor alpha

CC and IL-1beta from the monocytic cell line THP-1 (by similarity).

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.

CC -----

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CC -----

DR EMBL: AF218725; AAG44134.1; -

KW Cytokine; Glycoprotein; Signal.

FT SIGNAL 1 22

FT CHAIN 23 >178 INTERLEUKIN-17B.

FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT DISULFID 121 176 BY SIMILARITY.

FT DISULFID 126 178 BY SIMILARITY.

FT NON\_TER 178 178

SO SEQUENCE 178 AA; 20071 MW; 03D02D60BEC89A51 CRC64;

Query Match 14.7%; Score 157.5; DB 1; Length 178;

Best Local Similarity 29.5%; Pred. No. 5.9e-08;

Matches 46; Conservative 23; Mismatches 70; Indels 17; Gaps 4;

OY 45 GOAPPLRLGAKWGQALPVALLSSLEASHRGHRRPSATTQCPVLRPEVLEAD----- 100

DB 31 GOVREPLRPGP---HGVLDLVSRKYPARKREYERNLGENVAQLRNSSEPAKRCEVN 87

OY 101 ----THORSISPMWRVDTDEDRYPQKLAFAECLRCGIDARTGRTALNSVRLQSL 155

DB 88 LQWLMSNKRSLSPWGSINHDPSRIADLPPEARCLICGVNPPTMQEDRSVSPVF-SQ 146

OY 156 LVLR--RPRCSRDSGLPTPGAFAFHTEFIHVPVGCCTC 191

DB 147 VPVRRRLCPP-----PRGPCRRHVVMTJAVGCTC 178

RESULT 9

117B\_HUMAN

ID 117B\_HUMAN STANDARD; PRT; 180 AA.

AC 09DHF5;

DT 01-MAR-2002 (Rel. 41, Created)

DT 01-MAR-2002 (Rel. 41, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Interleukin-17 precursor (IL-17B) (Cytokine-like protein ZCYT07)

GN (Neuronal Interleukin-17 related factor) (Interleukin-20).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J.,

RA Martinez T., Hoffman R., O'Hara P.;

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-2010548; PubMed-10749887;  
 RA Shi Y., Dillisch S.J., Zhang J., Connolly K., Grzegorzewski K.J.,  
 RA Barber M.C., Wang W., Mathen K., Fisher C.L., Olsen H.,  
 RA Riden S.M., Knyazev I., Cho Y.H., Kao V., Wilkinson K.A.,  
 RA Carrell J.A., Ebner R.,  
 RA "A novel cytokine receptor-ligand pair. Identification, molecular  
 RA characterization, and in vivo immunomodulatory activity."  
 RA J. Biol. Chem. 275:19167-19176(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-2010548; PubMed-10639155;  
 RA Li H., Chen J., Huang A., Stinson J., Heldens S., Foster J., Dowd P.,  
 RA Gurney A.L., Wood W.L.,  
 RA "Cloning and characterization of IL-17B and IL-17C, two new members  
 RA of the IL-17 cytokine family." 97:773-778(2000).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Moore E.E., Presnell S., Garrigues U., Guilbot A., Leguenn E.,  
 RA Smith D., Yao L., Whitmore T.E., Gilbert T., Kresner R.E.,  
 RA "Identification of a novel IL-17 related factor: demonstration of  
 RA neuronal expression and evaluation as a candidate for the chromosome  
 RA 5q-linked form of Charcot-Marie-Tooth disease." 97:773-778(2000).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Zhang W., Wang J., Cao X.,  
 RA "Novel cytokine homology with interleukin-17." 97:773-778(2000).  
 RN [6]  
 RP Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 RA SEQUENCE FROM N.A.  
 RA Rieder M.O., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,  
 RA Nickerson D.A.,  
 RA Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Stimulates the release of tumor necrosis factor alpha  
 CC and IL-beta from the monocytic cell line THP-1.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed in adult pancreas, small intestine,  
 CC stomach, spinal cord and testis. Less pronounced expression in  
 CC prostate, colon mucosal lining, and ovary.  
 CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY  
 CC  
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 CC  
 DR EMBL: AF184969; AA01318.1;  
 DR EMBL: AF212311; AF28775.1;  
 DR EMBL: AF152098; AA28104.1;  
 DR EMBL: AF18727; AA04136.1;  
 DR EMBL: AF110385; AA039637.1;  
 DR EMBL: AF386077; AA03036.1;  
 DR MIM: 604627;  
 KM Cytokine; Glycoprotein; Signal.  
 KW SIGNAL  
 FT CHAIN 1 20  
 FT SIGNAL 1 20  
 FT CHAIN 21 180  
 FT DISULFID 121 176  
 FT DISULFID 126 178  
 FT CARBOHYD 75 75  
 FT SEQUENCE 180 AA; 20437 MW; F1B0BC1446D0B14A CRC64;  
 N-LINKED (GLCNAC. .) (POTENTIAL).  
 14.4%; Score 154.5; DB 1; Length 180;  
 Best Local Similarity 28.7%; Pred No. 1.1e-07;  
 Matches 45; Conservative 25; Mismatches 70; Indels 17; Gaps 4;

OY 45 GQAPHLARGAKMGQALPVVALVSSLEASHRGHERPSATTCQPVLRPEVLEAD---- 100  
 DB 31 GQGRGRLAPRP---HQVPLDVSARKRYARMEETERTIEEMVAQLNSSELRQKCEVN 87  
 OY 101 -----THORSTSPMYRYVDVDEDRYPOKLAFAECICRGCIDARTGRTAALNSVRLQSL 155  
 DB 88 LQWMSNRSLSPMGYSINHPDSRI PVDLPFARCLGICVNPFTMOBDRSMVSPVF-SQ 146  
 OY 156 IIVRRPGRSGSLPTPGAFATFEFIHPVGTCTV 192  
 DB 147 VPIRRRLCPPP-----PRPGCORARVMTTAVGTCTI 179  
 RESULT 10  
 IL17-RAT  
 ID IL17-RAT STANDARD: PRT: 150 AA.  
 AC 061453;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Interleukin-17 precursor (IL-17) (Cytotoxic T lymphocyte-associated  
 DE antigen 8) (CTLA-8).  
 GN IL17 OR CTLA8.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-93294300; PubMed-8390535;  
 RA Rouvier E., Luciani M.F., Mattei M.-G., Denizot F., Golstein P.,  
 RA "CTLA-8, cloned from an activated T cell, bearing an AU-rich messenger  
 RA RNA instability sequences, and homologous to a herpesvirus salm1ri  
 RA gene." 150:5445-5456(1993).  
 RN [2]  
 RP ORGANISM IDENTIFICATION.  
 RA MEDLINE-96194901; PubMed-8654948;  
 RA Yao Z., Timour M., Painter S., Fanslow W., Springs M.K.,  
 RA "Complete nucleotide sequence of the mouse CTLA8 gene." 150:5445-5456(1993).  
 RN [3]  
 RP SEQUENCE FROM N.A. AND ORGANISM IDENTIFICATION.  
 RA MEDLINE-97031826; PubMed-8877732;  
 RA Kennedy J., Rossi D.L., Zurewski S.M., Vega F. Jr., Kastelein R.A.,  
 RA Wagner J.L., Hannum C.H., Zlotnik A.,  
 RA "Mouse IL-17: a cytokine preferentially expressed by alpha beta TCR +  
 RA CD4-CD8-T cells." 16:611-617(1996).  
 CC -1- FUNCTION: INDUCES STROMAL CELLS TO PRODUCE PROINFLAMMATORY AND  
 CC HEMATOPOIETIC CYTOKINES (BY SIMILARITY).  
 CC -1- SUBUNIT: HOMODIMER. (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.  
 CC -1- CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO BE FROM MOUSE BUT, ON  
 CC THE BASIS OF SUBSEQUENT WORK (REF.2 AND REF.3), HAS BEEN SHOWN TO  
 CC BE OF RAT ORIGIN.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL: U13839; AAA37490.1;  
 KW Cytokine; Glycoprotein; T-cell; Antigen; Signal.  
 KW SIGNAL  
 FT CHAIN 1 17  
 FT SIGNAL 1 17  
 FT CHAIN 18 150  
 FT DISULFID 89 139  
 FT DISULFID 94 141  
 FT CARBOHYD 63 63  
 FT SEQUENCE 180 AA; 20437 MW; F1B0BC1446D0B14A CRC64;  
 N-LINKED (GLCNAC. .) (POTENTIAL).  
 14.4%; Score 154.5; DB 1; Length 180;  
 Best Local Similarity 28.7%; Pred No. 1.1e-07;  
 Matches 45; Conservative 25; Mismatches 70; Indels 17; Gaps 4;

FT CONFLICT 46 46 I -> L (IN REF. 3).  
SQ SEQUENCE 150 AA: 16876 MW: EF13F33EDF9D689F CRC64;

Query Match 13.8%; Score 148.5; DB 1; Length 150;  
Best Local Similarity 29.4%; Pred. No. 3.4e-07;

Matches 45; Conservative 20; Mismatches 55; Indels 33; Gaps 5;

OY 42 LPLGAPPLILARGAKMGQALPVALYSSLEASHGRHPSATTCQPYLRPEVLEADT 101  
DB 21 IQSSVCPAEANFNFLONKVKLVKINSLSKASSRRPS-----DY 61  
OY 102 HORSISPMRYRVDTEDEDRYPQKLARAECLRCGICDARTGRTAALNSVLLQSLYLRRR 161  
DB 62 LNRSTSPMTLSRNEDEPDRPSYIWEAQCRHRCVNAE-GKLDHNNNSVLIQOEIILVKRE 120  
OY 162 P--CSRDSGGLPTPGAFHFEFHVPGCTCV 192  
DB 121 PEKCG-----PFTFRVEKMLVGVCCTCV 142

## RESULT 11

IL17\_MOUSE STANDARD; PRT; 158 AA.

AC Q62386; Q60971;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Interleukin-17 precursor (IL-17) (Cytotoxic T lymphocyte-associated antigen 8) (CTLA-8).  
GN IL17 OR CTLA8.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BALB/C; TISSUE=Thymocytes;  
RX MEDLINE=97031826; PubMed=8877732;  
RA Kennedy J., Rossi D.L., Zurawski S.M., Vega F. Jr., Kastlein R.A., Wagner J.L., Hannum C.H., Zlotnik A.;  
RT "Mouse IL-17: a cytokine preferentially expressed by alpha beta TCR + CD4-CD8-T cells.";  
RL J. Interferon Cytokine Res. 16:611-617(1996).  
RN [2]  
RP SEQUENCE OF 12-158 FROM N.A.  
RC STRAIN=129/SV; TISSUE=T-cell;  
RX MEDLINE=96194901; PubMed=8654948;  
RA Yao Z., Timour M., Painter S., Fanslow W., Spriggs M.K.;  
RT "Complete nucleotide sequence of the mouse CTLA8 gene.";  
RL Gene 168:223-225(1996).  
CC -1- FUNCTION: INDUCES STROMAL CELLS TO PRODUCE PROINFLAMMATORY AND HEMATOPOIETIC CYTOKINES (BY SIMILARITY).  
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -1- TISSUE SPECIFICITY: RESTRICTED TO A SUBSET OF ACTIVATED T-CELLS.  
CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.  
CC -----  
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CC -----  
DR EMBL; U43088; AAB05222.1; -;  
DR EMBL; U35108; AAA93253.1; -;  
DR MGD; MGI:107364; 1117.  
KW Cytokine; Glycoprotein; T-cell; Antigen; Signal.  
FT SIGNAL 1 25 POTENTIAL.  
FT CHAIN 26 158 INTERLEUKIN-17.  
FT DISULFID 97 147 BY SIMILARITY.

FT DISULFID 102 149 BY SIMILARITY.  
FT CARBOHYD 71 71 N-LINKED (GLCNAC...)(POTENTIAL).  
SQ SEQUENCE 158 AA: 17490 MW: 3505C143435FA653 CRC64;

Query Match 13.8%; Score 148.5; DB 1; Length 158;  
Best Local Similarity 37.6%; Pred. No. 3.6e-07;

Matches 38; Conservative 13; Mismatches 35; Indels 15; Gaps 3;

OY 92 REEVELEADTHORSISPMRYRVDTEDEDRYPQKLARAECLRCGICDARTGRTAALNSVLL 151  
DB 65 RPSDYL-----NRSTSPMTLSRNEDEPDRPSYIWEAQCRHRCVNAE-GKLDHNNNSVLI 118  
OY 152 LOSLLYLRRRPPCSRDSSGLPTPGAFHFEFHVPGCTCV 192  
DB 119 QOEIILVKREPS-----CPFTFRVEKMLVGVCCTCV 150

## RESULT 12

HNF6\_HUMAN STANDARD; PRT; 465 AA.

AC Q9UBC0; Q9UMR6; Q99744;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hepatocyte nuclear factor 6 (HNF-6) (One cut domain family member 1).  
GN ONECUT1 OR HNF6A OR HNF6.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Futura H., Horikawa Y., Wang Y.-Q., Bell G.I.;  
RT "Isolation and characterization of the human hepatocyte nuclear factor 6 gene.";  
RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Futura H., Wang Y.-Q., Bell G.I.;  
RT "The sequence of human mRNA for the hepatocyte nuclear factor-6 alpha.";  
RL Submitted (APR-1997) to the EMBL/Genbank/DBJ databases.  
RN [3]  
RP SEQUENCE OF 1-368 FROM N.A., AND VARIANT ALA-75.  
RX MEDLINE=99420592; PubMed=10491763;  
RA Moeller A.M., Ek J., Durvieux S.M., Urhammer S.A., Clausen J.O., Elberg H., Hansen T., Rousseau G.G., Lemaigre F.P., Pedersen O.;  
RT "Hepatocyte nuclear factor-6: associations between genetic variability and type II diabetes and between genetic variability and estimates of insulin secretion.";  
RL Diabetologia 42:1011-1016(1999).  
RN [4]  
RP SEQUENCE OF 174-465 FROM N.A.  
RA Samadani U., Costa R.H.;  
RT "Yeast one-hybrid cloning of the partial human cDNA for hepatocyte nuclear factor 6.";  
RL Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.  
CC -1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR. BINDS THE CONSENSUS SEQUENCE 5'-DHATGATATGWD-3' ON A VARIETY OF GENE PROMOTERS SUCH AS THOSE OF HNF3B AND TTR. IMPORTANT FOR LIVER GENES TRANSCRIPTION.  
CC -1- SUBUNIT: BINDS DNA AS A MONOMER (BY SIMILARITY).  
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LIVER; LOWER EXPRESSION IN TESTIS AND SKIN.  
CC -1- SIMILARITY: BELONGS TO THE CUT FAMILY OF HOMEBOX PROTEINS.  
CC -----  
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CC EMBL: AF035581; AAD02033.1;  
 CC EMBL: AF035580; AAD02033.1; JOINED.  
 DR EMBL: U96173; AAD00826.1;  
 DR EMBL: Y17739; CAB00769.1;  
 DR EMBL: U77975; AAB61705.1;  
 DR TRANSFAC: T03286;  
 DR MIM: 604164;  
 DR InterPro: IPR003350; CUT.  
 DR InterPro: IPR001356; Homeobox.  
 DR Pfam: PF00046; CUT.1.  
 DR SMART: SM00389; HOX.1.  
 DR PROSITE: PS00027; HOMEBOX.1; FALSE\_NEG.  
 DR PROSITE: PS00071; HOMEBOX.2; 1.  
 KW Transcription regulation; Homeobox; DNA-binding; Nuclear protein;  
 KW Activator; Polymorphism.  
 FT DNA\_BIND 283 369 CUT.  
 FT DOMAIN 385 444 HOMEBOX.  
 FT DOMAIN 69 72 POLY-HIS.  
 FT DOMAIN 124 138 POLY-HIS.  
 FT DOMAIN 455 460 POLY-SER.  
 FT VARIANT 75 75 P->A.  
 FT CONFLICT 220 220 /FTID=VAR\_010729.  
 FT CONFLICT 284 284 A->T (IN REF. 3 AND 4).  
 FT CONFLICT 288 288 S->N (IN REF. 4).  
 FT CONFLICT 318 318 Q->H (IN REF. 4).  
 FT CONFLICT 386 386 R->K (IN REF. 4).  
 FT CONFLICT 386 386 K->O (IN REF. 4).  
 SQ SEQUENCE 465 AA; 51023 MW; F47F78957A6CF02 CRC64;

Query Match  
 Best Local Similarity 8.0%; Score 85.5; DB 1; Length 465;  
 Matches 48; Conservative 14; Mismatches 53; Indels 71; Gaps 11;

QY 18 AHHPDSLGRHSHGTPHCYSAEPLIGQAPP-----HLARAKKQCALPVALLVSSLEA 72  
 DB 220 AHHPRMLGRHGEQHLP--TSAGVPIPLGPPHHPHALLNAG--HGQLLGA----- 268  
 QY 73 ASHGRHHERPSAT-----TQCPVLRPEVLEADTHORSISPMRYRVDTDEDRY-- 120  
 DB 269 -----REPNSVYGAOVNSGNSGOMEINRKEVAO-----RITTELKRYSI 310  
 QY 121 POKLAFACLCR--GCID-----ARTGRETALNSVRL-----IQSLVLR 159  
 DB 311 POALFAQVLCRSQGTSLDLRNKPKMSKLKSGRETR--RMMKWLOEPEFQMSALR 366  
 QY 160 RRPCSR 165  
 DB 367 LAACKR 372

RESULT 13  
 HNF6\_MOUSE  
 ID HNF6\_MOUSE STANDARD; PRT; 465 AA.  
 AC 008755;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hepatocyte nuclear factor 6 (HNF-6) (One cut domain family member 1).  
 GN ONECT1 OR HNF6A OR HNF6.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Samadani U., Rausa F., Costa R.H.;  
 RT "Mouse hepatocyte nuclear factor-6 cDNA.";

RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR. BINDS THE CONSENSUS SEQUENCE  
 CC 5'-DHATGATGATWMD-3' ON A VARIETY OF GENE PROMOTERS SUCH AS THOSE  
 CC OF HNF3B AND TTR. IMPORTANT FOR LIVER GENES TRANSCRIPTION (BY  
 CC SIMILARITY).  
 CC -1- SUBUNIT: BINDS DNA AS A MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- SIMILARITY: CONTAINS 1 CUT DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE CUT FAMILY OF HOMEBOX PROTEINS.  
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CC EMBL: U95945; AAB53863.1;  
 DR TRANSFAC: T03296;  
 DR MGD: MGI:1196423; Onecut1.  
 DR InterPro: IPR003350; CUT.  
 DR InterPro: IPR001356; Homeobox.  
 DR Pfam: PF002376; CUT.1.  
 DR Pfam: PF00046; homeobox.1.  
 DR SMART: SM00389; HOX.1.  
 DR PROSITE: PS00027; HOMEBOX.1; FALSE\_NEG.  
 DR PROSITE: PS00071; HOMEBOX.2; 1.  
 KW Transcription regulation; Homeobox; DNA-binding; Nuclear protein;  
 KW Activator.  
 FT DNA\_BIND 283 369 CUT.  
 FT DNA\_BIND 385 444 HOMEBOX.  
 FT DOMAIN 69 72 POLY-HIS.  
 FT DOMAIN 124 138 POLY-HIS.  
 FT DOMAIN 450 460 POLY-SER.  
 SQ SEQUENCE 465 AA; 50952 MW; A770D27DD5AAC896 CRC64;

Query Match  
 Best Local Similarity 8.0%; Score 85.5; DB 1; Length 465;  
 Matches 48; Conservative 14; Mismatches 53; Indels 71; Gaps 11;

QY 18 AHHPDSLGRHSHGTPHCYSAEPLIGQAPP-----HLARAKKQCALPVALLVSSLEA 72  
 DB 220 AHHPRMLGRHGEQHLP--TSAGVPIPLGPPHHPHALLNAG--HGQLLGA----- 268  
 QY 73 ASHGRHHERPSAT-----TQCPVLRPEVLEADTHORSISPMRYRVDTDEDRY-- 120  
 DB 269 -----REPNSVYGAOVNSGNSGOMEINRKEVAO-----RITTELKRYSI 310  
 QY 121 POKLAFACLCR--GCID-----ARTGRETALNSVRL-----IQSLVLR 159  
 DB 311 POALFAQVLCRSQGTSLDLRNKPKMSKLKSGRETR--RMMKWLOEPEFQMSALR 366  
 QY 160 RRPCSR 165  
 DB 367 LAACKR 372

RESULT 14  
 HNF6\_RAT  
 ID HNF6\_RAT STANDARD; PRT; 465 AA.  
 AC P70512; 088755;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hepatocyte nuclear factor 6 (HNF-6) (One cut domain family member 1).  
 GN ONECT1 OR HNF6A OR HNF6.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]



RP SEQUENCE FROM N.A. (ISOFORM ALPHA).  
RC STRAIN-SPRAGUE-DAWLEY; TISSUE=Liver;  
RX MEDLINE=96382488; PubMed=8790352;  
RA Lemaigre F.P., Durvieux S.M., Truong O., Lannoy V.J., Hsuan J.J.,  
RA Rousseau G.G.,  
RT "Hepatocyte nuclear factor 6, a transcription factor that contains a  
RT novel type of homeobox domain and a single cut domain";  
RT Proc. Natl. Acad. Sci. U.S.A. 93:9460-9464(1996).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM BETA).  
RC STRAIN=Wistar;  
RX MEDLINE=98256275; PubMed=9593691;  
RA Lannoy V.J., Bueygin T.R., Rousseau G.G., Lemaigre F.P.,  
RT "Isoforms of hepatocyte nuclear factor-6 differ in DNA-binding  
RT properties, contain a bifunctional homeobox domain, and define the new  
RT ONECUT class of homeobox domain proteins";  
RT J. Biol. Chem. 273:13552-13562(1998).  
RN [3]  
RP CHARACTERIZATION.  
RX MEDLINE=97042457; PubMed=8887657;  
RA Samadani U., Costa R.H.;  
RT "The transcriptional activator hepatocyte nuclear factor 6 regulates  
RT liver gene expression";  
RT Mol. Cell. Biol. 16:6273-6284(1996).  
CC -1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR. BINDS THE CONSENSUS SEQUENCE  
CC 5'-DHAAATGATGATWD-3' ON A VARIETY OF GENE PROMOTERS SUCH AS THOSE  
CC OF HNF3B AND TTR. IMPORTANT FOR LIVER GENES TRANSCRIPTION. THE  
CC AFFINITY OF HNF-3ALPHA AND HNF-3BETA FOR DNA DIFFERS DEPENDING ON  
CC THE TARGET SEQUENCE.  
CC -1- SUBUNIT: BINDS DNA AS A MONOMER.  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA (SHOWN HERE) AND BETA;  
CC ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, BRAIN, SPLEEN AND TESTIS.  
CC -1- SIMILARITY: CONTAINS 1 CUT DOMAIN.  
CC -1- SIMILARITY: BELONGS TO THE CUT FAMILY OF HOMEBOX PROTEINS.  
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CC -----  
DR EMBL: Y96553; CA65389.1; -  
DR EMBL: Y14933; CA65150.1; -  
DR TRANSEFAC: T03257; -  
DR TRANSEFAC: T03258; -  
DR InterPro: IPR003350; CUT.  
DR InterPro: IPR001356; Homeobox.  
DR Pfam: PF02376; CUT; 1.  
DR Pfam: PF00046; homeobox; 1.  
DR SMART: SM00389; HOX; 1.  
DR PROSITE: PS00027; HOMEBOX\_1; FALSE\_NEG.  
DR PROSITE: PS50071; HOMEBOX\_2; 1.  
KW Transcription regulation; Homeobox; DNA-binding; Nuclear protein;  
KW Activator; Alternative splicing.  
FT DNA\_BIND 283 369 CUT.  
FT DNA\_BIND 385 444 HOMEBOX.  
FT DOMAIN 69 72 POLY-HIS.  
FT DOMAIN 124 138 POLY-HIS.  
FT DOMAIN 455 460 POLY-SER.  
FT VARSPLIC 368 368 A -> AESAMGGSVPSLRITSSGPGQSLVPPPL (IN  
FT ISOFORM BETA)  
SQ SEQUENCE 465 AA; 51067 MW; BD651267FD7AC896 CRC64;

Query Match 8.0%; Score 85.5; DB 1; Length 465;  
Best Local Similarity 25.8%; Pred. No. 1;  
Matches 48; Conservative 14; Mismatches 53; Indels 71; Gaps 11;

QY 18 AHNDPSLGRHSHGTPHCYSAREELPLGQAP-----HLIARQAKWGQALPALVALVSSLEA 72

DB 220 AHHPAALGRRHGEQHTLP--TSAGMVPINGLPRHPHAHLNAG--HGQLLGTA----- 268  
QY 73 ASHRGHEHPSRT-----TQCPVLRPEVLEADTHQHSISWRVRVTDDERY--- 120  
DB 269 -----REPNSVYGAQVNSGNSGQMEINTVEVAO-----RITTELKYSI 310  
QY 121 POKLAFACELCR--GCID-----ARTGRETAALNSVRL-----LQSLIVLR 159  
DB 311 PQALFQRYVLCNSQGLTSLDLRNRKPKSKLSGREIFR----RMMKWLOEPEQRMSALR 366  
QY 160 RRPCSR 165  
DB 367 LAACKR 372  
RESULT 15  
BRM\_DROME  
ID BRM\_DROME STANDARD; PRT; 1638 AA.  
AC P25439; Q9VUM5; Q9VUM6;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Homeotic gene regulator (Brahma protein).  
GN BRM OR CG5942 OR CG18438.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_Taxid=7227;  
RN [1]  
RP SEQUENCE FROM N.A. (LONG ISOFORM).  
RX MEDLINE=92154670; PubMed=1346755;  
RA Tamkun J.W., Deuring R., Scott M.P., Kissinger M., Pattatucci A.M.,  
RA Kaufman T.C., Kennison J.A.;  
RT "Brahma: a regulator of Drosophila homeotic genes structurally  
RT related to the yeast transcriptional activator SNF2/SWI2";  
RT Cell 68:561-572(1992).  
RN [2]  
RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).  
RC STRAIN=BERKELEY;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Ceoliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Morten J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abriil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Bertman B.P., Bhandari D., Bolshakov S.,  
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durkin K.J., Evangelista C.C., Ferraz C., Ferriere S., Fleischmann W.,  
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Nixon K., Nusskern D.R., Pacle J.M.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Massarman D.A., Weinstock G.M., Weisenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RT "The genome sequence of *Drosophila melanogaster*,"  
 RL Science 287:2185-2195(2000).  
 CC - FUNCTION: MAY ACT AS COACTIVATOR, ASSISTING ONE OR MORE DEDICATED  
 CC TRANSCRIPTIONAL ACTIVATORS OF ANT-C AND BX-C HOMEOTIC GENES. CAN  
 CC COUNTERACT THE REPRESSIVE EFFECT OF POLYCOMB PROTEIN.  
 CC - SUBCELLULAR LOCATION: Nuclear.  
 CC - ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A  
 CC SHORT FORM, MAY BE PRODUCED BY ALTERNATIVE SPLICING.  
 CC - DEVELOPMENTAL STAGE: HIGHEST EXPRESSION IN UNFERTILIZED EGGS AND  
 CC EARLY EMBRYOS.  
 CC - MISCELLANEOUS: 'BRAHMA' MEANS 'FATE' IN INDIA.  
 CC - SIMILARITY: CONTAINS 1 BROMODOMAIN  
 CC - SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: M85049; AAA19661.1;  
 DR EMBL: AE003529; AAF49557.1;  
 DR EMBL: AE003529; AAF49558.2;  
 DR PIR: A42091; A42091.  
 DR FLYBASE: FBgn0000212; brm.  
 DR InterPro: IPR001487; Bromodomain.  
 DR InterPro: IPR001410; DEAD.  
 DR InterPro: IPR001650; Helicase\_C.  
 DR InterPro: IPR000330; SNF2\_N.  
 DR Pfam: PF00439; bromodomain; 1.  
 DR Pfam: PF00271; helicase\_C; 1.  
 DR Pfam: PF00176; SNF2\_N; 1.  
 DR PRINTS: PR00503; BROMODOMAIN.  
 DR SMART: SM00297; BROMO; 1.  
 DR SMART: SM00487; DEXDC; 1.  
 DR SMART: SM00490; HELIC; 1.  
 DR PROSITE: PS00633; BROMODOMAIN.1; 1.  
 DR PROSITE: PS50014; BROMODOMAIN.2; 1.  
 KW Developmental protein; Transcription regulation; Nuclear protein;  
 KW Activator; Bromodomain; Helicase; ATP-binding; Alternative splicing.  
 FT DOMAIN 201 390 GLN/PRO-RICH.  
 FT NP\_BIND 798 805 ATP (POTENTIAL).  
 FT SITE 900 903 DECH BOX.  
 FT DOMAIN 1385 1392 ASP/GLU-RICH (ACIDIC).  
 FT DOMAIN 1394 1404 ARG/LYS-RICH (BASIC).  
 FT DOMAIN 1405 1410 ASP/GLU-RICH (ACIDIC).  
 FT DOMAIN 1415 1432 ARG/LYS-RICH (BASIC).  
 FT DOMAIN 1443 1513 BROMODOMAIN.  
 FT DOMAIN 1631 1638 POLY-ASP.  
 FT VARSPLIC 121 121 G -> A (IN SHORT ISOFORM).  
 FT VARSPLIC 122 222 MISSING (IN SHORT ISOFORM).  
 FT CONFLICT 687 687 D -> Y (IN REF. 1).  
 SO SEQUENCE 1638 AA; 185086 MW; A4494B29F4FE2E42A CRC64;

Query Match 7.9%; Score 84.5; DB 1; Length 1638;  
 Best Local Similarity 22.2%; Pred. No. 5.2; Mismatches 26; Indels 51; Gaps 8;  
 Matches 42; Conservative 26;

OY 22 PSIRGPHSHGTHCYSAEELPIGQAPH---LARGAKGQALPVALVSSLEAASHNG 77  
 DB 52 PGAYIGHPMOHGPP---GCGPPGHMPPHHOGMISKSGPMGMOMP---PTGPNMSPYQT 104  
 OY 78 RHRRPSATTOCCVLR-----PEEVLADTH--ORSISPMRYRVDTDDRYPOKIA 125  
 DB 105 HGMFPNAPTOPCIVSPGPGPPPPRRSSQENLHALQRAIDSMERKGIQEDPRYSQILA 164

OY 126 FAECICRCGICDARTGRTAALNSVRLLOS-----LVYLRPPCSRD----- 166  
 DB 165 -----MRATSKHQLNGNNGVNLRLTQTAVRLLARNKPIISMQNALQAAGQPP 215  
 OY 167 GSGJLTPGA 175  
 DB 216 GPPIGPPGA 224

Search completed: September 4, 2002, 01:59:50  
 Job time: 187 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2002, 01:55:48 : Search time 23.77 Seconds  
(without alignments)  
1433.740 Million cell updates/sec

Title: US-09-854-280-3  
Perfect score: 1073  
Sequence: 1 MTLPLGLFTWLHTCLAHN.....FHTFEHVPVGCCTCLPRSV 197

Scoring table: BIOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 562222 seqs, 172994929 residues  
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_fodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1073	100.0	197	4	Q9POM4
2	1065	99.3	197	4	Q9HC75
3	173	16.1	109	4	Q96P18
4	173	16.1	163	4	Q96PD4
5	169.5	15.8	180	11	Q99MY3
6	168.5	15.7	180	11	Q9QXR6
7	165.5	15.4	177	4	Q9H293
8	160.5	15.0	215	11	Q9H293
9	157.5	14.7	151	12	Q9CT14
10	157.5	14.7	178	11	Q9E016
11	157	14.6	141	6	Q95L56
12	154.5	14.4	180	4	Q9UHE5
13	136	12.7	78	4	Q9NUE6
14	129.5	12.1	111	11	Q9E017
15	110	10.3	148	5	Q19778
16	95.5	8.9	93	6	Q9BEH5

17	89.5	8.3	168	2	Q9XDC3	Q9XDC3 herbaspiril
18	89.5	8.2	521	12	Q9DP52	Q9DP52 meleagrid h
19	88.5	8.3	521	12	Q9E1H8	Q9E1H8 meleagrid h
20	88	8.2	1548	4	Q9MYW9	Q9MYW9 homo sapien
21	88	8.2	2161	4	Q9T566	Q9T566 homo sapien
22	86.5	8.1	389	10	Q9LE01	Q9LE01 arabidopsis
23	86	8.0	297	2	Q99391	Q99391 streptomyce
24	86	8.0	1098	11	Q9JL71	Q9JL71 mus musculu
25	84.5	7.9	317	4	Q9BTV9	Q9BTV9 homo sapien
26	84	7.8	179	10	Q93Z24	Q93Z24 arabidopsis
27	84	7.8	354	10	Q9SE51	Q9SE51 arabidopsis
28	82	7.6	313	3	Q9P795	Q9P795 schizosacch
29	82	7.6	415	2	Q9LGI3	Q9LGI3 oryza sativ
30	81.5	7.6	306	2	Q9LAD4	Q9LAD4 xanthomonas
31	81.5	7.6	380	5	Q9G5Z8	Q9G5Z8 caenorhabdi
32	81	7.5	553	16	Q9T1783	Q9T1783 pseudomonas
33	80.5	7.5	283	5	Q9W4E1	Q9W4E1 drosophila
34	80.5	7.5	358	5	Q9U123	Q9U123 leishmania
35	80.5	7.5	638	4	Q96LD4	Q96LD4 homo sapien
36	80	7.5	408	4	Q96H86	Q96H86 homo sapien
37	80	7.5	411	16	Q96313	Q96313 mycobacteri
38	79.5	7.4	681	5	Q9SRM4	Q9SRM4 drosophila
39	79.5	7.4	745	13	Q98S05	Q98S05 brachydanio
40	79.5	7.4	1406	5	Q9V4D4	Q9V4D4 drosophila
41	79.5	7.4	1406	5	Q9U110	Q9U110 drosophila
42	79.5	7.4	1408	5	Q9XZU7	Q9XZU7 drosophila
43	79	7.4	465	4	Q9BMD7	Q9BMD7 homo sapien
44	79	7.4	837	4	Q9Y4R8	Q9Y4R8 homo sapien
45	79	7.4	837	4	Q9BR21	Q9BR21 homo sapien

#### ALIGNMENTS

RESULT 1  
ID Q9POM4 PRELIMINARY: PRT: 197 AA.  
AC Q9POM4: 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
DR INTERLEUKIN 17C.  
DS Homo sapiens (Human).  
OS Homo sapiens: Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
RX MEDLINE=20105548; PubMed=10639155;  
RA Li H., Chen J., Huang A., Stinson J., Heidens S., Foster J., Dowd P.,  
RT Gurney A.L., Wood W.L.;  
RT "Cloning and Characterization of IL-17B and IL17C, Two New Members of  
the IL-17 Cytokine Family."  
RL Proc. Natl. Acad. Sci. U.S.A. 97:773-778(2000).  
SR EMBL: AF152099; AAF28105.1;  
SQ SEQUENCE 197 AA: 21765 MW; BAE0132E18DE7D08 CRC64;

Query Match	100.0%	Score 1073;	DB 4;	Length 197;
Best Local Similarity	100.0%	Pred. No. 2.1e-100;		
Matches 197; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MTLPLGLFTWLHTCLAHNPSLRHPSHCPTCYSAEELPLGAPPHLLARGKWKGO	60	
DB	1	MTLPLGLFTWLHTCLAHNPSLRHPSHCPTCYSAEELPLGAPPHLLARGKWKGO	60	
QY	61	ALPVALVSSLEASHRGHRRSPATTCVLRPEEVLADTHQRSISPMRYVDVDEDEY	120	
DB	61	ALPVALVSSLEASHRGHRRSPATTCVLRPEEVLADTHQRSISPMRYVDVDEDEY	120	
QY	121	PKLAFAECLRCGICDARTGRTETALNSVRLQLSLVLRPPCSRDGSLPPGAFAPFT	180	
DB	121	PKLAFAECLRCGICDARTGRTETALNSVRLQLSLVLRPPCSRDGSLPPGAFAPFT	180	

OY 181 EFTHVPGCTCVPRLSV 197  
 DB 181 EFTHVPGCTCVPRLSV 197

## RESULT 2

ID 09HC75 PRELIMINARY; PRT; 197 AA.  
 AC 09HC75;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE CYTOKINE CX2 PRECUSOR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhang W., He L., Wan T., Yuan Z., Cao X.;  
 RT "Novel human cytokine CX2 with homology to IL-17";  
 RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF142410; AAC27921.1;  
 SQ SEQUENCE 197 AA; 21784 MW; BAFBBA9F6314A768 CRC64;

Query Match 99.3%; Score 1065; DB 4; Length 197;  
 Best Local Similarity 99.5%; Pred. No. 1.3e-99;  
 Matches 196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MTLPLGLFLFWLHLCIAHNDPSLRGPHSHGTPHCYSAEELPLGQAPPHILANGAKWQ 60  
 DB 1 MTLPLGLFLFWLHLCIAHNDPSLRGPHSHGTPHCYSAEELPLGQAPPHILANGAKWQ 60  
 OY 61 ALPALVSLLEAASHRGHRRPSTATQCPVLRPEVELEADTHORSISPMWRVTDDEDRY 120  
 DB 61 ALPALVSLLEAASHRGHRRPSTATQCPVLRPEVELEADTHORSISPMWRVTDDEDRY 120  
 OY 121 POKIAFACLCRGCTDARTGRTAALNSVRLQSLIVLRPPCRDGGSLPTGAFAFHT 180  
 DB 121 POKIAFACLCRGCTDARTGRTAALNSVRLQSLIVLRPPCRDGGSLPTGAFAFHT 180  
 OY 181 EFTHVPGCTCVPRLSV 197  
 DB 181 EFTHVPGCTCVPRLSV 197

RESULT 3  
 ID 096P18 PRELIMINARY; PRT; 109 AA.  
 AC 096P18;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE M.L.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=21475866; PubMed=11591768;  
 RA Kawaguchi M., Onouchi L.F., Li X.-D., Essayan D.M., Schroeder J.,  
 RT "Identification of a Novel Cytokine, ML-1, and Its Expression in  
 RT Subjects with Asthma";  
 RL J. Immunol. 167:4430-4435(2001).  
 DR EMBL: AF332389; AAL14427.1;  
 SQ SEQUENCE 109 AA; 12327 MW; 52C5B34C36D30EB CRC64;

Query Match

16.1%; Score 173; DB 4; Length 109;

Best Local Similarity 39.0%; Pred. No. 5.7e-10;  
 Matches 39; Conservative 16; Mismatches 31; Indels 14; Gaps 3;

OY 97 LEADTHORSISPMWRVTDDEDRYPOKIAFACLCRGCTDARTGRTAALNSVRLQSL 156  
 DB 16 MSRNIESRSTSPMNTYVTPDPRNRPSEVVOACRNLGCTINQO-GKEDISMNSVPIQOETL 74

OY 157 VLRRR--PCSRDGSGLPTGAFAFHTEFIHVPVGTCTVLP 194  
 DB 75 VVRRKHGCS-----VSFOLEKVLVTGCTCTVLP 103

## RESULT 4

ID 096PD4 PRELIMINARY; PRT; 163 AA.  
 AC 096PD4;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE INTERLEUKIN-17F.  
 GN IL17F.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=21475830; PubMed=11591732;  
 RA Starnes T., Robertson M.J., Sledge G., Kelich S., Nakshatri H.,  
 RA Broxmeyer H.E., Thomas R.;  
 RT "Cutting Edge: IL-17F, a novel cytokine selectively expressed in  
 RT activated T cells and monocytes, regulates angiogenesis and  
 RT endothelial cell cytokine production";  
 RL J. Immunol. 167:4137-4140(2001).  
 DR EMBL: AF384857; AAK83350.1;  
 SQ SEQUENCE 163 AA; 18045 MW; E5287737C9E7BD46 CRC64;

Query Match 16.1%; Score 173; DB 4; Length 163;  
 Best Local Similarity 39.0%; Pred. No. 8.9e-10;  
 Matches 39; Conservative 16; Mismatches 31; Indels 14; Gaps 3;

OY 97 LEADTHORSISPMWRVTDDEDRYPOKIAFACLCRGCTDARTGRTAALNSVRLQSL 156  
 DB 70 MSRNIESRSTSPMNTYVTPDPRNRPSEVVOACRNLGCTINQO-GKEDISMNSVPIQOETL 128  
 OY 157 VLRRR--PCSRDGSGLPTGAFAFHTEFIHVPVGTCTVLP 194  
 DB 129 VVRRKHGCS-----VSFOLEKVLVTGCTCTVLP 157

RESULT 5  
 ID 099MY3 PRELIMINARY; PRT; 180 AA.  
 AC 099MY3;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE CYTOKINE CX1 PRECUSOR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=BAIB/C;  
 RC Zhang W., Cao X.;  
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF250308; AAK37427.1;  
 SQ SEQUENCE 180 AA; 20268 MW; AAEACF5PACA3D11E CRC64;

Query Match

15.8%; Score 169.5; DB 11; Length 180;



RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gastlisch S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mondavertis P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Suzuki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 RA Wyshak-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
 RA Hashizaki Y.,  
 RA "Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 409:685-690(2001).  
 DR EMBL AK003506: BAB2826.1;  
 DR MGD: MG1:1928397; 1117b.  
 FT NON\_TER 1  
 SO SEQUENCE 215 AA; 24196 MW; 21468E7E01A92154 CRC64;

Query Match 15.0%; Score 160.5; DB 11; Length 215;  
 Best Local Similarity 29.8%; Pred. No. 2; 2e-08;  
 Matches 48; Conservative 25; Mismatches 63; Indels 25; Gaps 5;

OY 45 GOAPPHLLARGAKWGALPVALVSSLEASHRGHHER-----PSATGCPVL 91  
 DB 66 GQRRPPLAAGP---HOVPLDLYSRVAPYARMERYENLGEVVAQLRNISEPAKKCEV- 121  
 OY 92 RPEVLEADPHORSISFWRYVDTERYPOKLAFAECICRGCIDARTGETALNSVRL 151  
 DB 122 ---NLQMLSNKRSLSWGSINHDPSRIPADLPEARCLGCVNPTTMDKSNMVSVPV 178  
 OY 152 LQSLVLRPPCSRDGSLPTGAFATFTFIHVPVGCCTV 192  
 DB 179 F-SQVPRRLCP---PRGPCRRVYMETIAGVCTCI 214

RESULT 9  
 ID 040633 PRELIMINARY; PRT; 151 AA.  
 AC 040633;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE INTERLEUKIN 17.  
 GN ORE13.  
 OS Salimline herpesvirus 2.  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Gammaherpesvirinae; Rhadinovirus.  
 OX NCBI\_TaxID=10381;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C-488;  
 RX MEDLINE=98037620; PubMed=9371569;  
 RA Knappe A., Hiller C., Thura M., Wittmann S., Hofmann H.,  
 RA Fleckenstein B., Fickenscher H.;  
 RT "The superantigen-homologous viral immediate-early gene ie14/vsag 1n  
 herpesvirus salimline-transformed human T cells";  
 RL J. Virol. 71:9124-9133(1997).  
 DR EMBL: Y13183; CAAV3627.1;  
 SO SEQUENCE 151 AA; 17189 MW; 49B2C9430C46BE32 CRC64;

Query Match 14.7%; Score 157.5; DB 12; Length 151;  
 Best Local Similarity 28.6%; Pred. No. 3e-08;  
 Matches 46; Conservative 22; Mismatches 58; Indels 35; Gaps 5;

OY 36 CSAEELPIGQAPPHLLARGAKWGALPVALVSSLEASHRGHHERPSATGCPVIRPEE 95  
 DB 18 CLYKSTTSNAQPRCLAA-----NNSEPRSVMTLSIRMMNTSSKRA----- 60  
 OY 96 VLEADPHORSISFWRYVDTERYPOKLAFAECICRGCIDARTGETALNSVRLQSL 155  
 DB 61 ----DYNNSTSPWTLYRNEDDQDRYPSVIMKACRYLGCYNA-DGVDYTHMSVPIQDEL 115

OY 156 LVLR--RPPCSRDGSLPTGAFATFTFIHVPVGCCTV 194  
 DB 116 LVVRKGNPCPN-----SFLERKLVYVGCCTVTP 145

RESULT 10  
 ID 09E016 PRELIMINARY; PRT; 178 AA.  
 AC 09E016;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DE NEURONAL INTERLEUKIN-17 RELATED FACTOR (FRAGMENT).  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 OX NCBI\_TaxID=10036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Moore E.E., Presnell S., Garrigues U., Guilbot A., Leguern E.,  
 RA Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.;  
 RT "Identification of a novel IL-17 related factor: Demonstration of  
 RT neuronal expression and evaluation as a candidate for the chromosome  
 RT 5q-linked form of Charcot-Marie-Tooth disease";  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF218725; AAG44134.1;  
 FT NON\_TER 178  
 SO SEQUENCE 178 AA; 20071 MW; 03D02D60BEC9A51 CRC64;

Query Match 14.7%; Score 157.5; DB 11; Length 178;  
 Best Local Similarity 29.5%; Pred. No. 3.6e-08;  
 Matches 46; Conservative 23; Mismatches 70; Indels 17; Gaps 4;

OY 45 GOAPPHLLARGAKWGALPVALVSSLEASHRGHHERPSATGCPVLRPEVLEAD----- 100  
 DB 31 GQVRPPLAAGP---HOVPLDLYSRVAPYARMERYENLGEVVAQLRNISEPAKKCEV 87  
 OY 101 -----THOSISFWRYVDTERYPOKLAFAECICRGCIDARTGETALNSVRLQSL 155  
 DB 88 LQMLSNKRSLSWGSINHDPSRIPADLPEARCLGCVNPTTMDKSNMVSVPV-F 146  
 OY 156 LVLRPPCSRDGSLPTGAFATFTFIHVPVGCCTV 191  
 DB 147 VVPRRLCP---PRGPCRRVYMETIAGVCTC 178

RESULT 11  
 ID 095L56 PRELIMINARY; PRT; 141 AA.  
 AC 095L56;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE INTERLEUKIN 17 (FRAGMENT).  
 GN IL17.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lee I.-K., Mwangi S.M., Olsen S., Kehrl M. Jr.;  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF416586; AAL08013.1;  
 FT NON\_TER 1  
 SO SEQUENCE 141 AA; 15945 MW; 94077A79DD803F3E CRC64;

Query Match 14.6%; Score 157; DB 6; Length 141;



RT "Identification of a novel IL-17 related factor: Demonstration of  
 RT neuronal expression and evaluation as a candidate for the chromosome  
 5q-linked form of Charcot-Marie-Tooth disease."  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF218724; AAG44133.1;  
 FT NON\_TER 1 1  
 FT NON\_TER 111 111  
 SO SEQUENCE 111 AA; 12628 MW; D1598392981BA867 CRC64;

Query Match 12.1% Score 129.5; DB 11; Length 111;  
 Best Local Similarity 37.8%; Pred. No. 14e-05;  
 Matches 28; Conservative 16; Mismatches 25; Indels 5; Gaps 2;

QY 101 THORISPMRYVDDEDEYPOKLAFAECICRCICIDARTGRTAALNSVRLQSLVLR 160  
 Db 30 SNKRSLSPMGYSINHDPSRIPEDLPARCLICGVNPFIMQEDRSMSVYPF-SQYPPVR 88  
 QY 161 RPSRDSGLPTPG 174  
 Db 89 RLCFQP---PRPG 98

RESULT 15  
 ID 019778 PRELIMINARY; PRT; 148 AA.  
 AC 019778:  
 DT 01-NOV-1996 (TRENBLrel. 01; Created)  
 DT 01-NOV-1996 (TRENBLrel. 01; Last sequence update)  
 DE 01-DEC-2001 (TRENBLrel. 19; Last annotation update)  
 GN F25D1.3 PROTEIN.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCB1\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kelly P.F.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA none;  
 RT "Genome sequence of the nematode C. elegans: A platform for  
 RT investigating biology."  
 RL Science 282:2012-2018(1998).  
 DR EMBL: Z73973; CAA98268.1;  
 SO SEQUENCE 148 AA; 16738 MW; ADB51FA38DFB3940 CRC64;

Query Match 10.3% Score 110; DB 5; Length 148;  
 Best Local Similarity 33.0%; Pred. No. 0.0018;  
 Matches 31; Conservative 17; Mismatches 34; Indels 12; Gaps 4;

QY 103 QRTSIPMYRYVDDEDEYPOKLAFAECICRCICIDARTGRTAALNSVRLQSLVLR 162  
 Db 51 ERALCPWDSRVNQESREPLIAESVLC-----KSRGSGTGAFCMPYVRVPIIRVS 104  
 QY 163 CSRDGSLPTPGAFAPHTERFHVPGCTCVLPSS 196  
 Db 105 CDR-STGL---NMYVRSLEI-TVGCHSVLPRT 132

Search completed: September 4, 2002, 01:59:18  
 Job time: 210 sec